

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 17, 2006, 10:49:16 ; Search time 1231 Seconds  
(without alignments)  
3347.359 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

Sequence: 1 MEYMPMEGGMGSRPTTSP.....QELSSNPPLATILIPPHARI 394

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5	
Ygapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-O=/abs/ABSSWEB.spool/US10733816/runat\_15092006\_085442\_15433/app\_query.fasta\_1  
-DB=N Geneseq -QFWT=fastcap -SUPFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p  
-USER=US10733816 @CGN 1.1 2019 @runat\_15092006\_085442\_15433 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	97.3	1260	13 ADT92556	Adt92556 Human gly
2	2024	97.3	1389	4 AAD1491	Aad1491 Human gly
3	2024	97.3	1389	10 ACA56816	Aca56816 Human sig

4	2024	97.3	1389	10	ADK11466	Adk11466 Human gly
5	2024	97.3	1389	12	ADI56612	Adi56612 Human pol
6	2024	97.3	1389	13	ADR40190	Adr40190 Human gly
7	2015	96.8	1525	10	ADB53390	Adb53390 Primary r
8	2015	96.8	1525	14	AEA62866	Aea62866 Rat glyco
9	2015	96.8	1972	2	AAQ67459	Aaq67459 Codes tau
10	2015	96.8	1972	10	ADB68895	Adb68895 Rat tau p
11	2013	96.7	1600	14	AE806397	Aee806397 Glycogen
12	2013	96.7	1815	5	ABV30267	Abv30267 Human pro
13	2012	96.7	1474	14	AEA62868	Aea62868 Rat glyco
14	2010	96.6	1503	12	ADI28892	Adi28892 Mouse gly
15	2010	96.6	2088	2	AAQ67458	Aaq67458 Codes tau
16	1996.5	95.9	1579	15	AE922755	Aef922755 Human GSK
17	1996.5	95.9	1639	9	ACC78383	Acc78383 Human gly
18	1996.5	95.9	1639	12	ADO49106	Ado49106 Human ded
19	1996.5	95.9	1639	13	ADS92934	Ads92934 Glycogen
20	1996.5	95.9	1639	13	ADR66574	Adr66574 Human pro
21	1996.5	95.9	1639	13	ADR66232	Adr66232 Human pro
22	1996.5	95.9	1639	13	ADU20924	Adu20924 Human gly
23	1996.5	95.9	1639	13	ADU05922	Adu05922 Novel bro
24	1996.5	95.9	1639	14	ADZ48946	Adz48946 Insulin s
25	1996.5	95.9	1639	14	AEB25736	Aeb25736 DNA encod
26	1996.5	95.9	1639	14	AEC34200	Aec34200 Human GSK
27	1996.5	95.9	1639	14	AEC81934	Aec81934 DNA encod
28	1996.5	95.9	1639	14	AER06395	Aee06395 Glycogen
29	1986	95.4	1230	10	ADR66952	Adr66952 Gene #42
30	1919	92.2	1501	14	AEE06401	Aee06401 Glycogen
31	1902.5	91.4	1540	14	AER06399	Aee06399 Glycogen
32	1634.5	78.5	1698	10	ADC99112	Adc99112 Human KPP
33	1609	77.3	1952	12	ADI61656	Adi61656 Human CDN
34	1609	77.3	1952	14	AEA43821	Aea43821 Human CDN
35	1609	77.3	2154	4	AAD14750	Aad14750 Human gly
36	1609	77.3	2169	6	ABK83893	Abk83893 Human CDN
37	1609	77.3	2169	9	ACC78382	Acc78382 Human gly
38	1609	77.3	2169	13	ADU18030	Adu18030 Human can
39	1609	77.3	2169	14	ADZ48945	Adz48945 Insulin s
40	1609	77.3	2169	14	AEC10094	Aec10094 Human gly
41	1609	77.3	2170	9	ACC78381	Acc78381 Human gly
42	1609	77.3	2189	14	AEC81933	Aec81933 DNA encod
43	1609	77.3	2374	12	ADQ21777	Adq21777 Human sof
44	1607	77.2	2155	10	ADB58321	Adb58321 Toxicity-
45	1607	77.2	2155	13	ADV41141	Adv41141 Rat cardi

ALIGNMENTS

RESULT 1

ADT92556  
ID ADT92556 standard; DNA; 1260 BP.

XX AC ADT92556;

DT 13-JAN-2005 (first entry)

XX DE Human glycogen synthase kinase-3-related coding sequence - SEQ ID 2.

XX DE neurodegenerative drug; glycogen synthase kinase-3; GSK-3;  
XX DE neurological disease; Parkinson's disease; Alzheimer's disease;  
XX KW Down's syndrome; cerebrovascular accident; stroke; spinal injury;  
XX KW Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;  
XX KW epilepsy; anxiety disorder; schizophrenia; depression;  
XX KW manic-depressive psychosis; gene; da.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT CDS 1..1260

FT /tag= a

FT /partial

FT /product= "Human glycogen synthase kinase-3-related

FT protein"

FT /note= "No stop codon is given"

XX

PN WO2004091663-A1.  
 XX 28-OCT-2004.  
 XX 16-APR-2004; 2004WO-JP005503.  
 XX 18-APR-2003; 2003JP-00114579.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Morishita T, Sakurada K, Suzuki K, Ikeda S;  
 XX WPI; 2004-784511/77.  
 XX P-PSDB; ADT92555.  
 XX Neurodegenerative drug for treating neurological disease e.g. Parkinson's  
 PT disease, Alzheimer's disease and Down's syndrome, contains substance  
 PT which inhibits activity of glycogen synthase kinase-3 as active  
 PT ingredient.  
 XX Disclosure; SEQ ID NO 2; 115pp; Japanese.  
 XX The invention comprises a neurodegenerative drug that inhibits the  
 CC activity of glycogen synthase kinase-3 (GSK-3). The neurodegenerative  
 CC drug of the invention is useful for treating neurological disease, such  
 CC as: Parkinson's disease, Alzheimer's disease, Down's syndrome,  
 CC cerebrovascular accident, stroke, spinal injury, Huntington's chorea,  
 CC multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety  
 CC disorder, schizophrenia, depression and manic-depressive psychosis. The  
 CC present human DNA sequence is used in the exemplification of the  
 CC invention.  
 XX SQ Sequence 1260 BP; 358 A; 300 C; 290 G; 312 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,34e-212 Length: 1260  
 Score: 2024.00 Matches: 384  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.3% Indels: 0  
 DB: 13 Gaps: 0

US-10-733-816-2 (1-394) x ADT92555 (1-1260)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 Db 1 ATGTTCAGGGGGCCAGAACCCACCTCTCTTTGGGAGAGCTGCAAGCCGGTGCAGACGCT 60  
 Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
 Db 61 TCAGCTTTTGGCAGCATGAAGTTTAGCAGAGACAAAGGACGCGCAAGGTGACACAGTG 120  
 Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
 Db 121 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAGCTATACAGACACTAAA 180  
 Qy 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLysCysAspSerGlyGlu 90  
 Db 181 GTGATTGGAAATGGATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 240  
 Qy 91 LeuValAlaIleLysValLysValLysValLysValLysValLysValLysValLys 110  
 Db 241 CTGTGCGCATCAAGAAGATATTTCAGGACAAAGAGATTTAAGAAATCAGAGACTCCAGTC 300  
 Qy 111 MetArgLysLysAspHisCysAsnIleValArgLysValTyrPhePheTyrSerSerGly 130  
 Db 301 ATGAGAAAGCTAGATCACTGTAAACATAGTCGATGCTGTTATTTCTCTCCTCAGCGGT 360  
 Qy 131 GluLysLysAspGluValTyrLysLysLysLysLysLysLysLysLysLysLysLys 150  
 Db 361 GAGAAGAAGATGAGGTCTATCTTAATCTGGTGTGAGCTATGTTCCGGAACAGTATAC 420  
 Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170

Db 421 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480  
 Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 Db 481 TATATGTATCAGCTGTTCCGAAGTTTAGCTATATCAATTCCTTTGGAAATCTCCCATCGG 540  
 Qy 191 AspIleLysProGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 210  
 Db 541 GATATTAAACCCGAGAACCTCTTTGGATCCCTGATCTGCTATATTAACAACTCTGTGAC 600  
 Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 Db 601 TTTGGAGTGCAGAACGAGCTGTCGAGGAGAACCAATGTTTCGTATATCTGTTCTCGG 660  
 Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 Db 661 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 720  
 Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAsp 270  
 Db 721 TGGTCTGCTGGCTGTGTGGCTGAGCTGTTACTAGGACCAACAATATTTCCAGGGGAT 780  
 Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290  
 Db 781 AGTGTGTGATCAGTTGGTAGAAATATCAAGTCTCTGGAACTCCACACAGGGAGCAA 840  
 Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
 Db 841 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 900  
 Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330  
 Db 901 TGGACTAAGGTCTTCCGACCCCAACTCCACCGAGGCAATTCACACTGTGTAGCCGCTG 960  
 Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
 Db 961 CTGGAGTATACACCAACTGCCCGACTAACCACTGGAAGCTTGTGGACACTTATTTT 1020  
 Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
 Db 1021 GATGAATTCAGGACCCAAATGTCAAAATCCAAATCCAAATGGCGAGACACACCTGCAC 1080  
 Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390  
 Db 1081 AACTTCACCACTCAAGAACTGTCAAGTAAATCCACTCTGCTACCATCTTATTTCTCCT 1140  
 Qy 391 HisAlaArgIle 394  
 Db 1141 CATGCTCGGATT 1152

RESULT 2  
 AAD11491  
 ID AAD11491 standard; DNA; 1389 BP.  
 XX  
 AC AAD11491;  
 XX 24-SEP-2001 (first entry)  
 XX Human glycogen synthase kinase 3-beta DNA #1.  
 XX Antisense; glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;  
 KW insulin regulation disorder; neurological disorder; Alzheimer's disease;  
 KW bipolar illness; inflammation; tumour; tau protein kinase 1; tpk-1;  
 XX human; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS /.\*tag= a  
 FT /product= "Glycogen synthase kinase 3-beta #1"

PN WO200152862-A1.  
 XX 26-JUL-2001.  
 XX 12-JAN-2001; 2001WO-US001085.  
 XX 19-JAN-2000; 2000US-00489765.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Butler MM, McKay R, Monia BP, Wyatt JR;  
 XX WPI; 2001-457510/49.  
 XX P-PSDB; ARE05998.  
 XX Novel antisense compounds, particularly antisense oligonucleotides for  
 PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for  
 PT diagnosing, treating neurological and insulin regulation disorders.  
 XX Example 13; Page 88-90; 106pp; English.  
 XX The invention relates to antisense compounds targetted to nucleic acid  
 CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau  
 CC protein kinase I (TPK-I)). The antisense compound is useful for  
 CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in  
 CC cells or tissues and for treating diseases or conditions associated with  
 CC the enzyme such as insulin regulation disorder, in particular diabetes  
 CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.  
 CC The antisense compound is also useful for diagnosing diseases associated  
 CC with the expression of glycogen synthase kinase 3-beta and for  
 CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour  
 CC formation and as a research reagent. The present sequence is human  
 CC glycogen synthase kinase 3-beta DNA  
 XX  
 SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.55e-212 Length: 1389  
 Score: 2024.00 Matches: 384  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.3% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-733-816-2 (1-394) x AAD11491 (1-1389)  
 QY 11 MetSerGlyValArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 DB 40 ATGTCAGGGCGGCCAGAACCCACTCTCTTTGGGAGAGCTGCAAGCCGGTGCAGAGCCT 99  
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
 DB 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACAGGACCGCAGCAAGGTGACACAGTG 159  
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70  
 DB 160 GTGGCAACTCTCGCGAGGGTCCAGACAGGCCACCAAGAGTCACTATACAGACACTAA 219  
 QY 71 ValIleGlyAsnGlySerPheGlyValValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
 DB 220 GTGATTGGAAATGGATCATTTGGTGGTATATCAAGCCCAAACTTTGTGATTGAGAGAA 279  
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 DB 280 CTGGTGGCCATCAAGAAGATTATTCAGGACAGAGATTTAAGATTCGAGAGCTCCAGATC 339  
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
 DB 340 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGGTTATTCTTCTACTCCAGTGGT 399  
 QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
 DB 400 GAGAAAGAAAGATGAGGTCTATCTTAATCTCGTGTGCTGAGCTATGTTCCGGAACAGTATAC 459  
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
 DB 460 AGAGTTTGCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519  
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 DB 520 TATATGTATCAGCTGTTCGAGAGTTAGCTATATCAATCTCTTTGGAAATCTGCCATCGG 579  
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 DB 580 GATATTAAACCCGACAGAACCTCTTTGTTGGATCTGTACTGTATTAAACCTCTGTGAC 639  
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 DB 640 TTTTGAAGTGCACAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 699  
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 DB 700 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759  
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
 DB 760 TGGTCTGCTGGCTGTGTGTTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 819  
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
 DB 820 AGTGTGTGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA 879  
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
 DB 880 ATCAGAGAATGAACCAACACTACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939  
 QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330  
 DB 940 TGGACTAAGGTCTTCCGACCCCGAAGCTCCACCGAGGCAATTCACCTGTAGCCGCTG 999  
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
 DB 1000 CTGGAGTATACACCAACTGCCGACCTAACACCACTGGAAGCTTGTGCACATTCATTTT 1059  
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370  
 DB 1060 GATGAATTCGGGACCCCAATGTCAAACATCCAAATGGGGGACACACCTGCACCTCTC 1119  
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProLeuAlaThrIleLeuIleProPro 390  
 DB 1120 AACTTCACCACTCAAGAACTGTCAAGTAAATCCACCTCTGGCTACCATCTTATTCCTCT 1179  
 QY 391 HisAlaArgIle 394  
 DB 1180 CATGCTCGGATT 1191  
 RESULT 3  
 ACA56816  
 ID ACA56816 standard; cDNA; 1389 BP.  
 XX  
 AC ACA56816;  
 XX  
 DT 06-JUN-2003 (first entry)  
 XX  
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1414.  
 XX  
 KW Human; probe; ss; array element; Parkinson's disease;  
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6500938-B1.  
 XX  
 PD 31-DEC-2002.  
 XX

PF 30-JAN-1998; 98US-00016434.  
 XX  
 PR 30-JAN-1998; 98US-00016434.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Au-Young J, Seilhamer JJ;  
 XX  
 DR WPI; 2003-352189/33.  
 XX  
 PT Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides.  
 XX  
 PS Claim 1; SEQ ID NO 1414; 65pp; English.  
 XX  
 CC The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signaling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=0650093981  
 XX  
 SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,55e-212 Length: 1389  
 Score: 2024.00 Matches: 384  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.3% Indels: 0  
 DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x ACA56816 (1-1389)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 Db 40 ATGTGAGGGGGCCAGACACCTCTCTTTGGGAGAGCTGCAAGCGCGTGCAGACGCT 99  
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysSerGlySerLysValThrVal 50  
 Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGCGGCGCAGCAAGGTGCAACAGTG 159  
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrThrLys 70  
 Db 160 GTGGCACTCTGGCGAGGGTCCAGACAGGCCACAGAGTGCAGTATACAGACACTAAA 219  
 QY 71 ValIleGlySerGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGlu 90  
 Db 220 GTGATTGGAAATGGATCAITTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGAGAA 279  
 QY 91 LeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 Db 280 CTGTGTCCTCATCAAGAAGATTTCAGACACAGAGATTTAAGATTCAGAGCTCCAGATC 339  
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130

Db 340 ATGAGAAAGCTAGATCACTGTAACTAGTCCGATTCGGTTATTCTTCTTACTCCAGTGGT 399  
 QY 131 GluLysLysAspGluValTyrLeuLeuValLeuValLeuValProGluThrValTyr 150  
 Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 459  
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
 Db 460 AGAGTTGCCAGACACTATAGTCCAGCCAAACAGACGCTCCCTGTGTATTTATGTCAAGTTG 519  
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 Db 520 TATATGATCACTGTTCGGAAGTTTAGCTATATCAITTCCTTTGGAATTCGCCATCGG 579  
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 Db 580 GATATTAAACCCGAGAACCTCTTTGGATCTCTGATACCTGCTGTATTAACACTCTGTGAC 639  
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 Db 640 TTTGGAGTGCAGAGCGCTGTCCGAGGAGAACCCAAATGTTTCGTATATCTGTCTCGG 699  
 QY 231 TyrTyrArgAlaProGluLeuPheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 Db 700 TACTATAGGGCACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 759  
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
 Db 760 TGGTCTCGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGAT 819  
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
 Db 820 AGTGGTGTGATCATGTTGTAGAAATATCAAGTCTCTGGAACTCCACACAGGGAGCAA 879  
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
 Db 880 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 939  
 QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330  
 Db 940 TGGACTTAAGGTCTTCCGACCCGAACTCCACCGAGGCAATTGCACTGTGTAGCCCTCTG 999  
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
 Db 1000 CTGGAGTATACCAACTGCCCCGACTAACACCACTGGAGAGCTTGTGCACATTCATTTTTT 1059  
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
 Db 1060 GATGAATTAACGGACCCAAATGTCAAAACATCCAAATGGGCGAGACACACCTGCACCTTC 1119  
 QY 371 AsnPheThrThrGlnGluSerSerAsnProProLeuAlaThrIleLeuIleProPro 390  
 Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCT 1179  
 QY 391 HisAlaArgIle 394  
 Db 1180 CATGCTCGAATT 1191

RESULT 4  
 ADK11466  
 ID ADK11466 standard; DNA; 1389 BP.  
 XX AC ADK11466;  
 XX 06-MAY-2004 (first entry)  
 XX Human glycogen synthase kinase 3 beta gene.  
 DE  
 KW da; gene; cytostatic; cardiovascular; immunosuppressive; nephrotropic;  
 KW antineumatic; aniarthritic; dermatological; antipsoriatic;  
 KW antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;  
 KW cardiovascular disorder; autoimmune disease; glomerulonephritis;  
 KW rheumatoid arthritis; dermatological disorder; psoriasis;



KW inflammatory disorder; malaria; emphysema; alopecia.

XX Homo sapiens.

XX WO2003040301-A2.

XX 15-MAY-2003.

XX 23-OCT-2002; 2002WO-GB0004780.

XX 05-NOV-2001; 2001GB-00026506.

XX 27-NOV-2001; 2001GB-00028384.

XX 11-FEB-2002; 2002GB-00003185.

XX (CYCL-) CYCLACEL LTD.

XX Deak P, Frenz L, Glover D, Midgley C;

XX WPI; 2003-441540/41.

XX P-PSDB; ADK11467.

XX New Drosophila polypeptides and polynucleotides, useful for diagnosing, preventing and/or treating disorders, such as cancer, glomerulonephritis, rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.

PS Example 27; Page 218; 265pp; English.

XX The invention relates to novel Drosophila species DNA sequences and their encoded proteins with their corresponding human homologues. The proteins or their encoding polynucleotides are useful in a method of prevention, treatment or diagnosis of a disease in an individual, and used to identify a substance capable of binding to the polypeptide or modulating the function of the polypeptide comprising incubating the polypeptide with a candidate substance and determining whether the substance binds to the polypeptide. The compositions are administered to an individual in need of such treatment. The method of diagnosis, in which the presence or absence of a polynucleotide is detected in a biological sample, comprises brining the biological sample containing the nucleic acid such as DNA or RNA into contact with a probe comprising a fragment of at least 15 nucleotides of the polynucleotide, and detecting any duplex formed between the probe and nucleic acid in the sample. The method also comprises providing an antibody capable of binding to the polypeptide, incubating a biological sample with the antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex comprising the antibody is formed. The disease comprises a proliferative disease such as cancer. The antibody or identified substance is also useful in inhibiting the function of a polypeptide and/or regulating a cell division cycle function. The diseases also include cardiovascular disorders, autoimmune diseases such as glomerulonephritis and rheumatoid arthritis, and dermatological disorders such as psoriasis, inflammatory, fungal, and parasitic disorders such as malaria, emphysema and alopecia. This sequence represents a human homolog gene for one of the Drosophila genes of the invention.

XX SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-55e-212 Length: 1389  
Score: 2024.00 Matches: 384  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.3% Indels: 0  
DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x ADK11466 (1-1389)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30

DB 40 ATGTCAGGGGGGCCAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGTGCAGCAGCT 99

QY 31 SerAlaPheGlySerMetIysValSerArgAspIysAspGlySerIysValThrVal 50

DB 100 TCAGCTTTTGGCAGCATGAAGATTAGCAGAGACAAGGACGCGAGAGGTGACAACAGTG 159

QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGlnValSerTyrThrAspThrLys 70  
DB 160 GTGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAAAGTCAGCTATACAGACACTAAA 219  
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
DB 220 GTGATTGGAAATGGATCATTTTGGTGGTATATCAAGCCAAACTTTGTGATTCAAGGAA 279  
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
DB 280 CTGGTCGCCATCAAGAAAGTATTTCAGGACAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339  
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
DB 340 ATGAGAAAGCTAGATCACTGTAACTAGTCCGATTGGTTTATTCTTCTCTCTCAGTGGT 399  
QY 131 GluLysIysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
DB 400 GAGAAGAAGATGAGGTCTATCTTAACTGGTGGCTGATGTTCGGAAACAGTATATAC 459  
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
DB 460 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTATGTCAGTGTG 519  
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
DB 520 TATATGTATCAGCTGTTCCGAAGTTAGCCTATATCCATTCTTCTTGGAACTGCGATCGG 579  
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
DB 580 GATATTAAACCGCAGAACCTCTTTGTTGGATCCTGTGATCTGTATTTAAAACACTGTGAC 639  
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
DB 640 TTTGGAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAAATGTTTCGATATATCTGTCTCGG 699  
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
DB 700 TACTATAGGCGACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759  
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
DB 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGAT 819  
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
DB 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGGAACCTCCAAAGGGAGCAA 879  
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
DB 880 ATCAGAGAAATGAACCCAAACTACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 939  
QY 311 TrpThrIysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330  
DB 940 TGGACTAAGGTCTTCCGACCCCACTCCACCGGAGGCAATTCGACTGTGTAGCCGCTG 999  
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
DB 1000 CTGGAGTATACACCAACTGCCCCGACTAACACCACTGGAGCTTGTGCACACTTATTATTTT 1059  
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
DB 1060 GATGAATTCGGGACCCAAATGTCAAACATCCAAATGGGGGAGACACACCTGCACCTCTC 1119  
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390  
DB 1120 AACTTCCACACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCTCTCT 1179  
QY 391 HisAlaArgIle 394  
DB 1180 CATGCTCGGATT 1191

RESULT 5	Query Match:	97.3%	Indels:	0
ADIS6612	DB:	12	Gaps:	0
ID ADIS6612 standard; DNA; 1389 BP.	US-10-733-816-2 (1-394) x ADIS6612 (1-1389)			
XX AC ADIS6612;				
XX 22-APR-2004 (first entry)				
XX DE Human polynucleotide probe #1414.				
XX KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;				
XX KW effector-like polypeptide; cancer; immunopathology; neuropathology;				
XX KW drug development; toxicology; carcinogenicity;				
XX KW signalling pathway polypeptide; adrenal gland; bladder; bone;				
XX KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;				
XX KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;				
XX KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.				
XX OS Homo sapiens.				
XX PN US2004010136-A1.				
XX PD 15-JAN-2004.				
XX PF 26-NOV-2002; 2002US-00305720.				
XX PR 30-JAN-1998; 98US-00016434.				
XX PA (INCYTE) INCYTE GENOMICS INC.				
XX PI Au-Young J, Seilhamer JJ;				
XX DR WPI; 2004-090520/09.				
XX PT New composition comprising polynucleotide probes, useful as array				
XX PT elements in a microarray for monitoring the expression of target				
XX PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic				
XX PT fragments.				
XX PS Claim 6; SEQ ID NO 1414; 73pp; English.				
XX CC The invention relates to a composition of polynucleotide probes				
XX CC comprising first polynucleotide probes comprising at least a portion of a				
XX CC gene encoding a receptor-like polypeptide, second polynucleotide probes				
XX CC comprising at least a portion of a gene encoding a transducing				
XX CC polypeptide and third polynucleotide probes comprising at least a portion				
XX CC of a gene encoding an effector-like polypeptide. The probes of the				
XX CC composition are useful as array elements in a microarray for monitoring				
XX CC the expression of target polynucleotides. The microarray is useful in the				
XX CC diagnosis and treatment of cancer, an immunopathology or a				
XX CC neuropathology. It can also be used for drug discovery and development,				
XX CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.				
XX CC Microarrays can also be used for monitoring the progression of diseases				
XX CC that may be associated with the altered expression of signalling pathway				
XX CC polypeptides. The composition can also be used to purify a subpopulation				
XX CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile				
XX CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of				
XX CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,				
XX CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or				
XX CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,				
XX CC epilepsy, Alzheimer's disease or depression. This sequence represents a				
XX CC human polynucleotide probe of the invention. Note: The sequence data for				
XX CC this patent did not form part of the printed specification but was				
XX CC obtained in electronic format directly from USPTO at				
XX CC seqdata.uspto.gov/sequence.html.				
XX SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;				
Alignment Scores:				
Pred. No.:	1.55e-212	Length:	1389	
Score:	2024.00	Matches:	384	
Percent Similarity:	100.0%	Conservative:	0	
Best Local Similarity:	100.0%	Mismatches:	0	

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30				
DB 40 ATGTGAGGGGGCCCAAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGTGCAGCAGCT 99				
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50				
DB 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGCAGCGCAGCAAGGTGACAACAGTG 159				
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrAspThrLys 70				
DB 160 GTGGCAACTCTCTGGCAGGGGTCCAGACAGCCACCAAGAAGTACGTATACAGACTAAA 219				
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90				
DB 220 GTGATTGGAAATGGATCATTTGGTGGTATATCAAGCCCAACTTTGTGATTCAGAGAA 279				
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110				
DB 280 CTGGTCGCATCAAGAAAGTATTTCAGAGCAAGAGATTTAAGAATCCAGAGCTCCAGATC 339				
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130				
DB 340 ATGAGAAAGCTAGATCACTGTAACTAGTCCGATTCGGTATTTCTTCTACTCCAGTGGT 399				
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150				
DB 400 GAGAACAGATGAGGTCTATCTTAATCTGGTCTGACTATGTTCCGGAAACAGTATAC 459				
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170				
DB 460 AGAGTTGCCAGACACTATAGTCAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519				
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190				
DB 520 TATATGTATCAGCTGTTCGAAAGTTAGCTTATCCATTCCTTTGGAAATCTCCCATCGG 579				
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210				
DB 580 GATATTAAACCCGACAGACCTCTTTGTTGGATCCTGTACTGTATTAATAACTCTGTGAC 639				
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230				
DB 640 TTTTGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCAATGTTTCGTATATCTCTCTCGG 699				
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerIleAspVal 250				
DB 700 TACTATAGGCACACAGATGTATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759				
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270				
DB 760 TGGTCTGCTGGCTGTGTGTGGCTAGCTGTACTAGGACCAACCAATATTTCCAGGGAT 819				
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290				
DB 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGAGCAA 879				
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310				
DB 880 ATCAGAGAAATGAACCCAACTACAGAAATTTAAATTCCTCAATTAAGGACATCTCT 939				
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330				
DB 940 TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGCAATTCACCTGTGTAGCGCTG 999				
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350				
DB 1000 CTGGAGTATACACCAACTGCCCGACCTAAACACCACCTGGAAGCTTGTGCACATTCATTTT 1059				

QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
 DB 1060 GATGAATTACGGGACCCAAATGTCAAACATCCAAATGGCGGAGACACACCTGCACTCTTC 1119  
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390  
 DB 1120 AACTTACCACCTCAAGAACGTCAAGTAATCCACTCTGGCTACCATCTTATCTCTCT 1179  
 QY 391 HisAlaArgile 394  
 DB 1180 CATGCTCGGATT 1191  
 RESULT 6  
 ADR40190  
 ID ADR40190 standard; cDNA; 1389 BP.  
 XX  
 AC ADR40190;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX Human glycoen synthase kinase 3 beta (GSK3beta) (1521) cDNA.  
 DE  
 XX  
 KW haematological; cytostatic; erythroid; anaemia; erythrocytosis;  
 KW bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;  
 KW T-cells; neutropenia; gene therapy; human; ss; gene;  
 KW glycoen synthase kinase 3 beta; GSK3beta.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 40..1302  
 FT /\*tag= a  
 FT /product= "Human glycoen synthase kinase 3 beta  
 FT (GSK3beta) (1521) protein"  
 XX  
 PN WO2004072242-A2.  
 XX  
 XX 26-AUG-2004.  
 XX  
 XX 05-FEB-2004; 2004WO-US003417.  
 XX  
 XX 05-FEB-2003; 2003US-0445241P.  
 PR 18-FEB-2003; 2003US-0448389P.  
 PR 20-MAR-2003; 2003US-0456320P.  
 PR 03-APR-2003; 2003US-0460279P.  
 PR 28-APR-2003; 2003US-0465924P.  
 PR 13-MAY-2003; 2003US-0470052P.  
 PR 26-AUG-2003; 2003US-0498106P.  
 PR 04-SEP-2003; 2003US-0500179P.  
 PR 15-SEP-2003; 2003US-0502909P.  
 PR 10-OCT-2003; 2003US-0510351P.  
 PR 17-OCT-2003; 2003US-0512380P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Kelly LM, Carroll JM, Farlow D, Healy A;  
 XX  
 XX WPI; 2004-625850/60.  
 DR P-PSDB; ADR40191.  
 DR  
 XX  
 XX Identifying a compound capable of treating a hematological disorder  
 PT comprises combining a compound to be tested with a polypeptide related  
 PT with the disorder under conditions suitable for binding of the test  
 PT compound to the polypeptide.  
 XX  
 XX Disclosure; SEQ ID NO 71; 321pp; English.  
 PS  
 XX  
 CC The invention relates to a novel method for identifying a compound  
 CC capable of treating a hematological disorder which comprises combining a  
 CC compound to be tested with a specific polypeptide under conditions  
 CC suitable for binding of the test compound to the polypeptide. The method  
 CC of the invention has hematological and cytostatic applications and may  
 CC be useful for identifying compounds for treating a hematological

CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,  
 CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and  
 CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds  
 CC identified may be utilised during gene therapy procedures. The current  
 CC sequence is that of a human haematological disorder-related cDNA of the  
 CC invention.  
 XX  
 SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,55e-212 Length: 1389  
 Score: 2024.00 Matches: 384  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.3% Indels: 0  
 DB: 13 Gaps: 0  
 US-10-733-816-2 (1-394) x ADR40190 (1-1389)  
 QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 DB 40 ATGTCAGGCGCGGCCAGAACCCACCTCTTTGCGGAGAGCTGCAAGCGGTGCAGACGCT 99  
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
 DB 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGCAGCAGCGCAGGAGGTGACACAGTG 159  
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
 DB 160 GTGGCACTCTTGGCGAGGCTCCAGCAGGCCACAGAGTGCAGTATACAGACACTAAA 219  
 QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuLysCysAspSerGlyGlu 90  
 DB 220 GTGATTGGAAATGCATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGGAA 279  
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 DB 280 CTGGTCGCATCAAGAAAGTATTGCGAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC 339  
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
 DB 340 ATGAGAAAGCTAGATCACTGTACATAGTCCGATTTGGTATTCTTCTTCTACTCCAGTGT 399  
 QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
 DB 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTCGGAACAGTATAC 459  
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
 DB 460 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 519  
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 DB 520 TATATGTATCAGCTGTTCGAGTTAGCTATATCAATCTCTTGGAAATCTGCCATCGG 579  
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 DB 580 GATATTAAACCGCAGAACCTCTTGTGGATCTCTGATCTGTATTTAAACTCTGTGAC 639  
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 DB 640 TTTTGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 699  
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 DB 700 TACTATAGGCGCACAGATTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGA 759  
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlnProIlePheProGlyAsp 270  
 DB 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACAATATTTCCAGGGGAT 819  
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290

```
Db      820 AGTGGTGGATCAGTTGGTAGAAATAATCAAGTCTCTGGAACTCCCAACAGGAGCAA 879
Qy      291 ILAArgGluMetAenProAenTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
      |||
Db      880 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
Qy      311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
      |||
Db      940 TGGACTAAGGTCTTCCAGCCCGCAACTCCACCGAGGCAATGGACATGTGTAGCCGTCG 999
Qy      331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
      |||
Db      1000 CTGGAGTATACCAACTGCCCGACTAACCACTGGAAGCTGTGTGCACATTCATTTTT 1059
Qy      351 AspGluLeuArgAepProAenValLysHisProAenGlyArgAepThrProAlaLeuPhe 370
      |||
Db      1060 GATGAATACCGGACCCCAATGTCAAAATCCAAATGGCGGAGACACACCTGCACCTTTC 1119
Qy      371 AenPheThrThrGlnGluLeuSerSerAenProLeuAlaThrIleLeuIleProPro 390
      |||
Db      1120 AACTTACCACCTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCCTTATTCCTCT 1179
Qy      391 HisAlaArgIle 394
      |||
Db      1180 CATGCTCGGATT 1191

RESULT 7
ADBS3390
ID      ADBS3390 standard; DNA; 1525 BP.
XX      AC      ADBS3390;
XX      DT      04-DEC-2003 (first entry)
XX      DE      Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3932.
XX      KW      toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX      KW      toxicity marker; toxicity progression; drug screening;
XX      KW      primary rat hepatocyte toxicity modelling; gene; ds.
XX      OS      Rattus norvegicus.
XX      PN      WO2003065993-A2.
XX      PD      14-AUG-2003.
XX      PF      04-FEB-2003; 2003WO-US003482.
XX      PR      04-FEB-2002; 2002US-0353171P.
XX      PR      13-MAR-2002; 2002US-0363534P.
XX      PR      08-APR-2002; 2002US-0370248P.
XX      PR      10-APR-2002; 2002US-0371134P.
XX      PR      10-APR-2002; 2002US-0371135P.
XX      PR      10-APR-2002; 2002US-0371150P.
XX      PR      11-APR-2002; 2002US-0371413P.
XX      PR      13-APR-2002; 2002US-0373601P.
XX      PR      19-APR-2002; 2002US-0373602P.
XX      PR      22-APR-2002; 2002US-0374139P.
XX      PR      08-MAY-2002; 2002US-0378370P.
XX      PR      09-MAY-2002; 2002US-0378652P.
XX      PR      09-MAY-2002; 2002US-0378653P.
XX      PR      09-MAY-2002; 2002US-0378655P.
XX      PR      09-JUL-2002; 2002US-0394230P.
XX      PR      09-JUL-2002; 2002US-0394253P.
XX      PR      04-SEP-2002; 2002US-0407688P.
XX      PR      28-JAN-2003; 2003US-0442900P.
XX      PA      (GENE-) GENE LOGIC INC.
XX      PI      Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
XX      PI      Elashoff M;
XX      WPI; 2003-731472/69.
```

```
XX      PS      Claim 44; SEQ ID NO 3932; 874pp; English.
XX      CC      The present invention describes a method for determining whether a
      CC      compound induces a toxic effect on a tissue or cell. The method comprises
      CC      preparing a gene expression profile of a tissue or cell sample exposed to
      CC      the compound, and comparing the gene expression profile to a database
      CC      comprising data or information on the Tox mean and non-Tox mean value.
      CC      The method is useful for predicting or identifying at least one toxic
      CC      effect, particularly hepatotoxicity, of a test or unknown compound. The
      CC      genes listed in the specification are useful as diagnostic or toxicity
      CC      markers for the prediction or identification of the physiological state
      CC      of tissue or cell sample that has been exposed to a compound, or to
      CC      identify or predict the toxic effects of a compound or an agent. These
      CC      may also be used as markers for monitoring toxicity progression or for
      CC      drug screening. The present sequence represents a primary rat hepatocyte
      CC      toxicity modelling related gene sequence from the present invention.
XX      SQ      Sequence 1525 BP; 459 A; 372 C; 351 G; 343 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.75e-211      Length:      1525
Score:      2015.00      Matches:      386
Percent Similarity:      98.0%      Conservative:      0
Best Local Similarity:      98.0%      Mismatches:      2
Query Match:      96.8%      Indels:      6
DB:      10      Gaps:      1

US-10-733-816-2 (1-394) x ADBS3390 (1-1525)
Qy      7      GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
      |||
Db      110 GAAGGAAAGGTGAATCGAGAGAGCCATCATCTCGGGGCGACCGAGAACCACTCTCTT 169
Qy      21      AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
      |||
Db      170 GCGGAGAGCTGCAAGCCAGTCGACGAGCCCTTCAGCTTTTGGTAGCATGAAAGTTAGCAGA 229
Qy      41      AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60
      |||
Db      230 GATAAGATGGCAGCAAGGTAAACACAGTGGTGGCACTCTCGACAGGGTCTCTGACAGG 289
Qy      61      ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
      |||
Db      290 CCACAGGAAGTCAGTTACACAGACACTAAAGTCATTGGAATGGTCACTTTGGTGTGTA 349
Qy      81      TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
      |||
Db      350 TATCAAGCCAAACTTTGTGACTCAGGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409
Qy      101      LysArgPheLysAenArgGluLeuGlnIleMetArgLysLeuAspHisCysAenIleVal 120
      |||
Db      410 AAGCGATTAAAGAACCGAGAGCTCCAGATCATGAGAAGCTAGATCACTGTAACTAGTC 469
Qy      121      ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
      |||
Db      470 CGATTGGGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTAACCTG 529
Qy      141      ValLeuAspTyrValProGluThrValTyrArgValAlaIleArgHisTyrSerArgAlaLys 160
      |||
Db      530 GTGCTGGACTATGTTCGGGAAACAGTGTACAGAGTCGCCAGACACATATAGTCGAGGCCAAG 589
Qy      161      GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
      |||
Db      590 CAGACACTCCCTGTGATCTATGTCAGAGTTGATATGATACCGCTGTTCAGAAAGTCTAGCC 649
Qy      181      TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAenLeuLeuAsp 200
      |||
```



Db 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATGTATGACAGCTGTTCAGAACTCTAGCC 649

Qy 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAenLeuLeuLeuAsp 200

Db 650 TATATCCATTCCCTTGGATCTGCATCGAGACATTAAACCCAGAACCTCTTGCTGGAT 709

Qy 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220

Db 710 CCTGATACAGCTGATTAAACCTCTGGACTTTGGAAAGTGCAAGAGCTGGTCCGAGGA 769

Qy 221 GluProAenValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240

Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGCGCACAGAGCTGATCTTTGA 829

Qy 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260

Db 830 GCCACCGATTACAGCTCTAGTATAGATGTATGTCTCGAGCTGTGTGTGGCTGAATTG 889

Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280

Db 890 TTGCTAGGACCAACCAATATTCTCTGGGGACAGTGTGTGATCAGTTGGTGGAAATAA 949

Qy 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAenProAenTyrThrGlu 300

Db 950 AAGTCTCTAGNACACCAACAGGGAGCAATTTAGAGAAATGAACCCAAATTTATACAGAA 1009

Qy 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProAthrPro 320

Db 1010 TTCAAAATCCCCCAATCAAGGCACATCTCTGGAGCAAGCTCTTTCGGCCCGCACTCCA 1069

Qy 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340

Db 1070 CCAGAGCAATTCGCACCTGTGTAGCCGTCTCTCGAGTACACGCGACCCGCGCTAAACA 1129

Qy 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAenValLysHis 360

Db 1130 CCACTGGAGCTGTGCACATTCATTTTGTGATTAATTCGGNCCCAATGTCAACTA 1189

Qy 361 ProAenGlyArgAspThrProAlaLeuPheAenPheThrThrGlnGluLeuSerSerAgn 380

Db 1190 CCAAAATGGCGGAGACACACCTGCCCTCTCAACTTTTACCACCTCAAGAACTGTCAAGTAAC 1249

Qy 381 ProProLeuAlaThrIleLeuIleProProHisAlaArgIle 394

Db 1250 CCACCTCTGGCCACCATCTTATCCCTCTCACGCTCGGATT 1291

RESULT 9

AAQ67459

ID AAQ67459 standard; cDNA to mRNA; 1972 BP.

XX

AC AAQ67459;

XX

AC

XX

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX

XX Codes tau-protein kinase I (TPK-I), Alzheimer's disease.

DE

XX

XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease; ds.

XX

XX Rattus rattus.

XX

XX Key Location/Qualifiers

FT mat\_peptide 140..1400

FT /\*tag= a

XX

XX EP616032-A2.

XX

XX

PD 21-SEP-1994.

XX

XX 01-MAR-1994; 94EP-00103057.

PF

XX

XX 02-MAR-1993; 93JP-00041160.

PR

XX

XX 22-MAR-1993; 93JP-00085143.

PR 02-AUG-1993; 93JP-00191246.

XX

PA (MITU ) MITSUBISHI KASEI CORP.

PA (MITU ) MITSUBISHI CHEM CORP.

XX

PI Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A;

PI Sato S;

XX

DR WPI; 1994-287181/36.

DR P-PSDB; AAR61327.

XX

XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-protein providing means for prevention and treatment of Alzheimer's disease.

PT

PT

XX

PS Claim 4; Page 18; 30pp; English.

XX

CC AAQ67459 codes for a newly isolated tau-protein kinase I enzyme (TPK-I), shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a rat fetus brain cDNA library, and was expressed in insect cells. TPK-I acts specifically on tau-protein, which is thought to be involved in Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped that the characterisation of TPK-I may lead to development of new agents for the prevention and therapy of these diseases. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 1972 BP; 614 A; 453 C; 427 G; 477 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 2,59e-211 Length: 1972

Score: 2015.00 Matches: 386

Percent Similarity: 98.0% Conservatives: 0

Best Local Similarity: 98.0% Mismatches: 2

Query Match: 96.8% Indels: 6

DB: 2 Gaps: 1

US-10-733-816-2 (1-394) x AAQ67459 (1-1972)

Qy 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20

Db 110 GAAGGAAAAGGTGAATCGAAGAGCCATCATCTCGGGCGCAGCAACCACTCTCTTT 169

Qy 21 AlaGluSerCysLysProValGlnProSerAlaPheGlySerMetLysValSerArg 40

Db 170 GCGGAGAGCTGCAAGCCAGTCGACAGCCCTTACGCTTTTGGTAGCATGAAGTTAGCAGA 229

Qy 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60

Db 230 GATAAAGATGGCAGCAAGGTAACCAAGTGTGGCAACTCTCTGGACAGGGTCTCTGACAGG 289

Qy 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80

Db 290 CCACAGGAAGTCAGTTACACAGACACTAAAGTCATTGGAAATGGGTCAATTGGTGGTA 349

Qy 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysValLeuGlnAsp 100

Db 350 TATCAAGCCCAACTTTGTGACTCAGGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409

Qy 101 LysArgPheLysAenArgGluLeuGlnIleMetArgLysLeuAephHisCysAenIleVal 120

Db 410 AAGCGATTTAAGAACCCGAGAGCTCCAGATCATGAGAAGCTAGATCACTGTAAATAGTC 469

Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140

Db 470 CGATTGCGGTATTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTAACCTG 529

Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaAArgHisTyrSerArgAlaLys 160

Db 530 GTCTGGAATATGTTCCGAAAACAGTGTACAGAGTCCGACAGACATATAGTCGAGGCCAAG 589

Qy 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180

Db 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTATGATGCTGTTCAGAAAGTCTAGCC 649







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QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 473 CTGGTCGCCATCAAGAAGATTTCGAGGACAAGAGATTTAAGAAATCGAGAGCTCCAGATC 532
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
DB 533 ATGAGAAAGCTAGATCCTCTGTAACATAGTCGGAATGGCTATTCTCTACTCAGTGGT 592
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 593 GAGAAAGAGATCAGGCTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 652
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
DB 653 AGAGTTGCCACAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 712
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 713 TATATGATCAGCTGTTCCGAAGTTTAGCTTATATCCATTCCTTTGGATCTGCCATCGG 772
QY 191 AspLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 773 GATATTAAACCGCAGAACCTCTTGTGGATCCTGATACCTGCTGTATTATAAACTCTGTGAC 832
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
DB 833 TTTTGAAGTCAAGACGCTGGTCCGAGGAGAACCAATGTTTCGTATATCTGTCTCGG 892
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyValThrAspTyrThrSerSerIleAspVal 250
DB 893 TACTATAGGCACACAGATGTGATCTTTGGAGCCACTGATTATACCTCTAGTAGATGTA 952
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
DB 953 TGGTCTGCTGCTGTGTGGTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGAT 1012
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
DB 1013 AGTGGTGTGGATCAGTTGGTGAATAATCAAGTCTCTGGGAACCTCCAAACAGGAGCAA 1072
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
DB 1073 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 1132
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
DB 1133 TGGACTAAGTCTTCCGACCCCGACTCCACCGAGGCAATTCGACTGTGTAGCCGCTCG 1192
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
DB 1193 CTGGAGTATACACCAACTGCCCGACTAACACCACTGGAAGCTTTGTGCACATTCATTTT 1252
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
DB 1253 GATGNAATTACGGACCCCAATGTCAAACTACCAAAATGGGCGAGACACACCTGCACCTTC 1312
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
DB 1313 AACTTACCACTCAGNACTGTCAAGTAATCCACCTCTGGCTACCATCTCTATTCTCTCT 1372
QY 391 HisAlaArgIle 394
DB 1373 CATGCTCGGATT 1384
RESULT 12
ID ABV30267
XX ABV30267 standard; cDNA; 1815 BP.
AC ABV30267;
XX
XX
DT 16-SEP-2002 (first entry)
XX
```

DE Human prostate expression marker cDNA 30258.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6569; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 1815 BP; 528 A; 406 C; 420 G; 458 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.: 3,79e-211 Length: 1815  
Score: 2013.00 Matches: 383  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 96.7% Indels: 0  
DB: 5 Gaps: 0

US-10-733-816-2 (1-394) x ABV30267 (1-1815)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnPro 30

DB 325 AYGTCAGGGGGGCCAGAACCCACTCTTTTGGAGAGCTGCAAGCGGTGACAGCCT 384

QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50

DB 385 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACACAGGACGCGCAAGGTGACACAGTG 444

QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70

DB 445 GTGGCAACTCTCTGGGCGAGGTCAGACAGGCCCAAGAGTTCAGCTATACAGACTAAA 504

QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90

DB 505 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCCAACTTTGTGATTCAGGAA 564

```
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 565 CTGGTCCCATCAAGAAAGATTATGACGAGCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 624
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
DB 625 ATGGAAGAAGCTAGATCACTGTAACATAGTCGGATTGGGTATTTCCTACTCCAGTGGT 684
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 685 GAGAAGAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 744
QY 151 ArgValAlaAlaGhiTyrSerArgAlaLysGluThrLeuProValIleTyrValLysLeu 170
DB 745 AGAGTTGCCAGACACTATAGTCGAGCCAAACACAGCGCTCCCTGTGATTTATGTCAAGTTG 804
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 805 TATATGTAATCAGCTGTTCCGAAGTTAGCCTATATCCATTCCTTTGGAACTCGCCATCGG 864
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 865 GATATTAAACCGCAGAACCTCTGTTGGATCCTGATACCTGCTGTATTAAAACTCTGTGAC 924
QY 211 PheGlySerAlaLysGlnLeuValAlaTqGlyGluProAsnValSerTyrIleCysSerArg 230
DB 925 TTTGGAAAGTCAAGACAGCTGGTCCGAGGAGAACCCCAATGTTTGTATATCTGTCTCTCGG 984
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
DB 985 TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGTGA 1044
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
DB 1045 TGGTCTGCTGGCTGTGTGGTGGCTGAGCTGTACTAGGCAACCAATATTTCAGGGGGAT 1104
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
DB 1105 AGTGGTGTGATCAGTTGGTAGAAATTAATCAAGTCTCTGGAACTCCAAACAGGGAGCAA 1164
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
DB 1165 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTCCTCDAATTAAGGCACATCCT 1224
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
DB 1225 TGGACTAAGGTCTTCCGACCCGAACTCCACCGAGGCAATTGCACTGTGTAGCCGCTG 1284
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
DB 1285 CTGGAGTATACCAACTGCCCGACTAACCCACTGGAAGCTGTGACACATTATTTTTT 1344
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
DB 1345 GATGAATACGGGACCCCAATGTCAAACTACCAATAGGCGAGACACACCTGCACTCTTC 1404
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
DB 1405 AACCTTCAACCTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCCT 1464
QY 391 HisAlaArgIle 394
DB 1465 CATGCTCGGATT 1476
RESULT 13
ID AEA62868 standard; DNA; 1474 BP.
XX AEA62868;
AC AEA62868;
DT 25-AUG-2005 (first entry)
XX XX Rat glycogen synthase kinase 3-beta (GSK3-beta) DNA sequence - SEQ ID 17.
```

```
XX antisense therapy; bone; bipolar disorder; neuroleptic; mania; antimanic;
KW Alzheimers disease; neuroprotective; nootropic; diabetes; antidiabetic;
KW leukopenia; immunostimulant; hyperproliferation; cytostatic;
KW glycogen synthase kinase 3-beta; GSK3-beta; ds.
XX Rattus norvegicus.
XX WO2005054518-A2.
XX 16-JUN-2005.
XX 06-DEC-2004; 2004WO-US041019.
XX 04-DEC-2003; 2003US-0527172P.
XX 04-DEC-2003; 2003US-0527173P.
XX 04-DEC-2003; 2003US-0527174P.
XX 04-DEC-2003; 2003US-0527370P.
XX 04-DEC-2003; 2003US-0527397P.
XX 04-DEC-2003; 2003US-0527420P.
XX 03-DEC-2004; 2004US-00004762.
XX (ISIS-) ISIS PHARM INC.
XX Bennett FC, Butler WM, Dean NM, Dobie KW, Finger J, Jain R;
XX McKay R, Monia BP, Myers K;
XX WPI; 2005-435410/44.
XX Novel oligomeric compound having nucleobases targeted to bone growth
XX modulator nucleic acid, and inhibiting expression of bone growth
XX modulator e.g., sclerostin, useful for inhibiting expression of bone
XX growth modulator in animal.
XX Example 4; SEQ ID NO 17; 357pp; English.
XX The invention comprises oligomeric compounds which are targeted to a
XX nucleic acid molecule encoding a bone growth modulator chosen from
XX dickkopf-1 (DKK-1), glycogen synthase kinase 3-beta, (GSK3-beta), s-
XX frizzled-related protein 1 (sFRP-1), sclerostin, transducer of ERBB1, and
XX arc-c. The oligomeric compound of the invention is capable of inhibiting
XX the expression of the bone growth modulator. The oligomeric compound of
XX the invention is useful for inhibiting the expression of a bone growth
XX modulator in a biological fluid, cell or tissue. The oligomeric compound
XX of the invention is further useful in the treatment of bipolar disorder,
XX mania, Alzheimer's disease, diabetes, leukopenia, sclerosteosis, and
XX hyperproliferative disorders. The present nucleic acid represents a rat
XX GSK3-beta DNA sequence.
XX Sequence 1474 BP; 436 A; 365 C; 341 G; 332 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 3,56e-211 Length: 1474
Score: 2012.00 Matches: 385
Percent Similarity: 98.0% Conservative: 1
Best Local Similarity: 97.7% Mismatches: 2
Query Match: 96.7% Indels: 6
DB: 14 Gaps: 1
US-10-733-816-2 (1-394) x AEA62868 (1-1474)
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```
QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
DB 85 GAAGGAAAAGGTGAATCGAAGAGCGCATCATGTGCGGCGGAGCCGAGAACCACTCTCTTT 144
QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
DB 145 GCGGAGAGCTGCAAGCCAGTCAGCAGCCTTCAGCTTTTGTAGCATGAAAGTTAGCAGA 204
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
DB 205 GATAAAGATGGCAGCAAGGTAAACACAGTGTGTGGCAACTCTCTGGACAGGGTCTCTGACAG 264
```

Qy 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80  
Db 265 CCACAGGAAGTCAGTTTACACAGACACTAAAGTCAATGGAAATGGGTCTATTGGTGTGTA 324  
Qy 81 TyrGlnAlaLysLeuCyAspSerGlyGluLeuValAlaLysLysValLeuGlnAsp 100  
Db 325 TATCAGCCAACTTTGTGACTCAGGAGAACTGGTGCCATCAGAAAGTTCTTCAGGAC 384  
Qy 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120  
Db 385 AAGCGATTTAAGAACCCAGAGCTCCAGATCATGATGAGAAAGCTAGATCACTGTAACATAGTC 444  
Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140  
Db 445 CGATTGGCGGTATTTCTTACTACGATGGCGAGAAAGATGAGGTCTACCTTTAACTG 504  
Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160  
Db 505 GTGCTGGACTATGTTCCGGAAACAGTGTACAGAGTCGCCAGACACTATAGTCGAGCCAG 564  
Qy 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180  
Db 565 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACAGCTGTTCAGAAAGTCTAGCC 624  
Qy 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200  
Db 625 TATATCCATTCTTTGGGATCTGCATCGAGACATTAAACCCACAGAACCTCTTGCTGGAT 684  
Qy 201 ProAspThrAlaValLeuLysLeuCyAspPheGlySerAlaLysGlnLeuValArgGly 220  
Db 685 CCGTATACAGCTGATTAAACTCTCGACCTTTGGAAAGTGCNAAGCAGCTGGTCCGAGGA 744  
Qy 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240  
Db 745 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGCGACCCAGAGCTGATCTTTGA 804  
Qy 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260  
Db 805 GCCACCATACAGCTCTAGTATAGATATGTGTCTGCAGGCTGTGTGTGGCTGAATTG 864  
Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280  
Db 865 TTGCTAGAACCAACATATTCTTCGGGGACAGTGTGTGATCAGTTGGTGGAAATATA 924  
Qy 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300  
Db 925 AAGTCTCTAGAACACCAACAGGAGCAATTAGAGAAATGAACCAATTATACAGAA 984  
Qy 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320  
Db 985 TTCAAATTTCCCAAAATCAAGGCACATCTTTGGACGAAGGTCTTTTCGGCCCGCACTCCA 1044  
Qy 321 ProGluAlaIleAlaLeuCySerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340  
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Qy 381 ProProLeuAlaThrIleLeuIleProHisAlaArgile 394  
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RESULT 14  
ADI28892  
ID ADI28892 standard; cdna; 1503 BP.  
XX  
AC ADI28892;

XX 22-APR-2004 (first entry)  
DT Mouse glycogen synthase kinase 3-beta coding sequence.  
XX  
DE  
XX Mouse; Glycogen synthase kinase 3-beta; cardiomyopathy;  
KW cardiovascular-gen.; cardiac; antianginal; gene therapy; transgenic;  
KW myosin; enzyme; gene; ss.  
XX  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 33..1295  
FT /\*tag= a  
FT /product= "Murine GSK-3beta"  
XX  
PN WO2004005474-A2.  
XX  
XX 15-JAN-2004.  
XX  
XX 03-JUL-2003; 2003WO-US021035.  
XX  
XX 03-JUL-2002; 2002US-0393525P.  
XX  
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX Robbins J;  
XX  
XX WPI; 2004-091352/09.  
XX P-PSDB; ADI28893.  
XX  
XX New isolated nucleic acid molecule having inducible cardiac-preferred  
PT expression, useful for diagnosing or treating cardiac diseases, including  
PT ischemic heart disease, angina pectoris, myocardial infarction and  
PT endocarditis.  
XX  
XX Claim 29; SEQ ID NO 7; 69pp; English.  
XX  
XX The present sequence is that of cDNA encoding a constitutively active  
CC form of murine glycogen synthase kinase 3 beta (GSK-3beta). GSK-3beta is  
CC a serine/threonine kinase that may affect cellular processes including  
CC development, differentiation and proliferation. When dephosphorylated at  
CC Ser-9, the kinase activity of GSK-3beta is constitutively active. The  
CC invention relates to methods of altering cardiac-preferred expression in  
CC transgenic animals. An animal cell or animal is stably transformed with  
CC an expression cassette comprising a cardiac-preferred promoter ADI28896  
CC operably linked to a nucleotide sequence of interest, e.g. GSK-3beta.  
CC Expression cassettes, host cells and transgenic animals are provided. The  
CC transgenic animals may have an altered susceptibility to cardiopathology  
CC making them useful for identifying anti-cardiopathic compounds. The  
CC cardiopathology is especially a cardiomyopathy such as familial  
CC hypertrophic cardiomyopathies, dilated cardiomyopathies, peripartum  
CC cardiomyopathy, restrictive cardiomyopathies, ischaemic heart disease,  
CC angina pectoris, myocardial infarction, hypertensive heart disease and  
CC endocarditis (claimed).  
XX  
SQ Sequence 1503 BP; 450 A; 361 C; 340 G; 352 T; 0 U; 0 Other;  
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Db 153 GTGGCAACTCTCTGGCCAGGCTCTGACAGGCCACAGGAAGTCAGTTATATACAGACAGAAA 212
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 213 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCTGGAGAA 272
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Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 393 GAGAAGAAAGATGAGTCTACCTTAACCTGGTGTGACTATGTTCCGGAGACAGTGTAC 452
Qy 151 ArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 453 AGAGTCCCCAGACACTATAGTCGAGCCAGAGACACTCCCTGTGATCTATGTCAGTTG 512
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 513 TATATGTATCAGCTGTTTCAGAGTCTAGCTATATATCCATTCCTTTGGAACTCGCCATCGA 572
Qy 191 AspIleLysProGlnAnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 573 GACATTAAACACACAGAACCTCTTGTGGATCCTGATACAGCTGTATTAAACACTCTGTGAC 632
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
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Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 873 ATTAGAGAAATGAACCCAAATTTATACAGAAATTCCTCAAAATCAAGGCACATCCT 932
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 933 TGGCAAAAGGTCTTTCCGCCCCGAACTCCACAGAGGCAATTGCACTGTGCGAGCGCTG 992
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 993 CTGAGATACACACTACGCCCCGGCTAACCACTGGAGCTGTGGACATTCATTTTTC 1052
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
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Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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AC AAQ67458;
XX 25-MAR-2003 (revised)
DT 21-APR-1995 (first entry)
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XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
PH mat_peptide 616..1885
FT /*tag= a
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XX EP616032-A2.
XX
XX 21-SEP-1994.
XX
XX 01-MAR-1994; 94BP-00103057.
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XX 02-MAR-1993; 93JP-00041160.
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XX 22-MAR-1993; 93JP-00085143.
XX
XX 02-AUG-1993; 93JP-00191246.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX (MITU ) MITSUBISHI CHEM CORP.
XX
XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A;
XX Sato S;
XX WPI; 1994-287181/36.
XX P-PSDB; AAR61326.
XX
XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-
XX protein providing means for prevention and treatment of Alzheimer's
XX disease.
XX Claim 4; Page 14; 30pp; English.
XX
XX AAQ67458 codes for a newly isolated tau-protein kinase I enzyme (TPK-1),
XX shown in AAR61326 (compare to rat AAR61327). The cDNA was cloned from a
XX rat fetus brain cDNA library, and was expressed in insect cells. TPK-I
XX acts specifically on tau-protein, which is thought to be involved in
XX Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped
XX that the characterisation of TPK-I may lead to development of new agents
XX for the prevention and therapy of these diseases. (Updated on 25-MAR-2003
XX to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 2088 BP; 656 A; 452 C; 434 G; 546 T; 0 U; 0 Other;

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US-10-733-816-2 (1-394) x AAQ67458 (1-2088)

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Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
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Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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Qy 391 HisAlaArgIle 394
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2015	96.8	1972	2	US-08-602-264A-2 Sequence 2, Appli
4	2015	96.8	1972	3	US-08-461-018A-2 Sequence 2, Appli
5	2015	96.8	1972	3	US-09-216-958-2 Sequence 2, Appli
6	2010	96.6	2088	2	US-08-602-264A-1 Sequence 1, Appli
7	2010	96.6	2088	3	US-08-461-018A-1 Sequence 1, Appli
8	2010	96.6	2088	3	US-09-216-958-1 Sequence 1, Appli

9	1609	77.3	1952	3	US-09-566-921-24 Sequence 24, Appli
10	1609	77.3	2154	3	US-09-488-856A-3 Sequence 3, Appli
11	1245	59.8	1636	3	US-09-578-194-6 Sequence 6, Appli
12	1244.5	59.8	1814	3	US-09-347-801-9 Sequence 9, Appli
13	1244.5	59.8	1814	3	US-09-854-731-9 Sequence 9, Appli
14	1240	59.6	1673	3	US-09-347-801-15 Sequence 15, Appli
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17	1165.5	56.0	1429	3	US-09-854-731-13 Sequence 13, Appli
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23	622	29.9	12394	3	US-09-488-856A-10 Sequence 10, Appli
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25	485	23.3	3823	3	US-09-949-016-4276 Sequence 4276, Ap
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36	460.5	22.1	2213	3	US-09-023-655-1037 Sequence 1037, Ap
37	459	22.1	1635	3	US-09-417-197-112 Sequence 112, App
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39	457	22.0	1467	2	US-08-176-820A-3 Sequence 3, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 3, Application US/09489765A  
; Patent No. 6323029  
; GENERAL INFORMATION:  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES  
; FILE REFERENCE: RTS-0124  
; CURRENT APPLICATION NUMBER: US/09/489,765A  
; CURRENT FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 3  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)...(1302)  
US-09-489-765A-3

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Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCTGATATCTGCTGATTTAAATCTCTGTGAC 639  
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 640 TTTGGAAAGTGCAGAGCTGTTCCGAGGAGAACCCATGTTTCGTATATCTGTTCTCGG 699  
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 700 TACTATAGGCACCCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 759  
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 760 TGGTCTGCTGCTGTGTGTGGCTGAGCTGTATTAGGACCAACCAATATTTCAGGGGAT 819  
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
Db 820 AGTGGTGGATCAGTTGGTAGAAATATCATAGTCTCTGGAACTCCACACAGGAGCAA 879  
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 880 ATCAGAGAAATGAACCCCAACATACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939  
Qy 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330  
Db 940 TGGACTAAGGTCTTCCAGCCCGAACCTCCACCGAGGCAATTTGCACCTGTGTAGCCGCTG 999  
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 1000 CTGAGTATACACCAACTGCCCGACTAACCACTGGAGAGCTTGTGCACATTCATTTT 1059  
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1060 GATGAATTACGGGACCCAAATGTCAAAATCATCAAAATGGCGGAGACACACCTGCACTCTTC 1119

Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390  
Db 1120 AATTTCACCACTCAGAACTGTCAAGTATATCCACTCTGGCTACCATCTTATTCCTCT 1179  
Qy 391 HisAlaArgIle 394  
Db 1180 CATGCTCGGATT 1191  
RESULT 2  
US-09-016-434-1414  
; Sequence 1414, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1414:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1389 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9529236  
; US-09-016-434-1414  
Alignment Scores:  
Pred. No.: 1.67e-237 Length: 1389  
Score: 2024.00 Matches: 384  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.3% Indels: 0  
DB: 3 Gaps: 0  
US-10-733-816-2 (1-394) x US-09-016-434-1414 (1-1389)  
Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
Db 40 ATGTTCAGGGCGGCCAGAACCCCTCTTTGGGAGAGCTGCAGCCGGTGCGAGCCT 99  
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACGAGCGCAGCAAGGTGACACAGTG 159

Qy 51 ValalaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
Db 160 GTGGCAACTCTCGGGCAGGGTCCAGACAGGCCCAAGAAAGTCAGCTATACAGACACTAAA 219  
Qy 71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCyAspSerGlyGlu 90  
Db 220 GTGANTGGAAATGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTGAGGAGAA 279  
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 280 CTGGTCCCATCAAGAAGATTATGCAGACACAGAGATTAAAGATCGAGAGCTCCAGATC 339  
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCGGATTGCTTATTTCTTACTCCAGTGGT 399  
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGATATAC 459  
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 460 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519  
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
Db 520 TATATGTATCAGCTGTTCCGAAGTTTACGCTATATCCATCTCTTGGAAATCTGCCATCGG 579  
Qy 191 AspileLysProGlnLeuLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 580 GATATTAAACCGGAGAACCTCTTGTGGATCCTGATCTGCTGATTAAACACTCTGGAC 639  
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 640 TTTGGAAGTCMAAGCAGCTGCTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCGG 699  
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 700 TACTATAGGACCCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759  
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGCAACCAATATTTCCAGGGGAT 819  
Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290  
Db 820 AGTGTGTGGATCAGTTGGTAGAAATATCAAGTCTCTGGNACTCCACAGGGAGCAA 879  
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 880 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 939  
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330  
Db 940 TGGACTAAAGTCTTCCGACCCGAACTCCACCGAGGCAATTCGACTGTGTAGCCGCTG 999  
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 1000 CTGGATATACCAACTGCCGACCTAACCACTGGAAGCTTGTGGACATTCATTTTTT 1059  
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1060 GATGAATTACGGGACCCCAATATGTCAACATCCAAATGGCGGAGACACACCTGCACCTTC 1119  
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390  
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCACTTATTTCTCCT 1179  
Qy 391 HisAlaArgIle 394  
Db 1180 CATGCTCGGATT 1191

## RESULT 3

US-08-602-264A-2  
; Sequence 2, Application US/08602264A  
; Patent No. 5837853  
; GENERAL INFORMATION:  
; APPLICANT: Akihiko TAKASHIMA et al.  
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR  
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE  
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WENDEROTH, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 144 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,264A  
; FILING DATE: February 20, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/204,091  
; FILING DATE: March 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1972 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to genomic RNA  
; ORIGINAL SOURCE:  
; ORGANISM: rat  
US-08-602-264A-2

Alignment Scores:  
Pred. No.: 3,82e-236 Length: 1972  
Score: 2015.00 Matches: 386  
Percent Similarity: 98.0% Conservative: 0  
Best Local Similarity: 98.0% Mismatches: 2  
Query Match: 96.8% Indels: 6  
DB: 2 Gaps: 1

US-10-733-816-2 (1-394) x US-08-602-264A-2 (1-1972)

Qy 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20  
Db 110 GAAGGAAAGGTGAATCGAGAGAGCCATCATGTGGGGGCGACGAGAACCACTCTCTTT 169  
Qy 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40  
Db 170 GCGAGAGCTGCAAGCCAGTCGACAGAGCTTACGTTTGTAGCATGAAAGTTAGCAGA 229  
Qy 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60  
Db 230 GATAAAGTGGCAAGCAAGGTAAACACAGATGTGTGGCAACTCTCTGCAGAGGTCTCTGACG 289  
Qy 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80  
Db 290 CCACAGGAAGTCAGTTACACAGACACTAAAGTCAATTGGAAATGGGTCAATTGGTGTGGTA 349

QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaLysValLeuGlnAsp 100  
Db 350 TATCAAGCCAACTTTGTGACTCAGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409  
QY 101 LysArgPheLysAsnArgGluLeuGlnMetArgLysLeuAspHisCysAsnIleVal 120  
Db 410 AAGGATTTAAGAACCCAGAGCTCCAGATCATGGAAGCTAGATCACTGTAACTAGTC 469  
QY 121 ArgLeuArgTyrPhePheTyrSerGlyLysLysAspGluValTyrLeuAsnLeu 140  
Db 470 CGATTGGGTATTTCTTACTCGAGTGGCAGAGAAGATGAGGTCTACCTTAACCTG 529  
QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160  
Db 530 GTGCTGGACTATGTTCCGGAACAGTGTACAGAGTCCGACACATAGTTCGAGCCAAAG 589  
QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180  
Db 590 CAGACATCCCTGTGATCTATGTCTAGTTGTATATGACCAGCTGTTCAAGATCTAGCC 649  
QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200  
Db 650 TATATCCATTCTTTGGGATCTGCATCGACATTAACACACAGAACCTCTTGCTGGAT 709  
QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220  
Db 710 CCTGATACAGCTGATTAATAAATCTGCGACTTTGGAAAGTGCAAGACAGCTGGTCCGAGGA 769  
QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240  
Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGCGCACAGAGCTGATCTTTGGA 829  
QY 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260  
Db 830 GCCACCGATTACAGCTCTAGTATAGATGTATGGTCTCAGGCTGTGTGGCTGAATTG 889  
QY 261 LeuLeuGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280  
Db 890 TTGCTAGGACAACCAATATTTCTCTGGGGACAGTGGTGTGATCAGTTGGTGGAAATAATA 949  
QY 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300  
Db 950 AAGTCTCTAGAACACCAACAGGAGCAATATTAGAGAAATGAACCCAAATATTACAGAA 1009  
QY 301 PheLysPheProGlnIleLysAlaHisProThrPheLysValPheArgProArgThrPro 320  
Db 1010 TTCAAAATTCCTCCCAATCAAGGCACATCTTGGACGAAGTCTTTTCGGCCCGCAACTCCA 1069  
QY 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340  
Db 1070 CCAGAGCAATTCGCACCTGTGTAGCCGTCCTCTGGAGTACAGCGACCGCCGCGCTAAACA 1129  
QY 341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360  
Db 1130 CCACTGGAGCTGTGCACATTCATTTTGTGAAATTAACGGACCCCAATGTCAACTA 1189  
QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380  
Db 1190 CCAATGGCGAGACACACCTGCCCTCTCAACTTTTACCCTCAAGAACTGTCAAGTAAC 1249  
QY 381 ProProLeuAlaThrIleLeuIleProHisAlaArgIle 394  
Db 1250 CCACCTTGGCCCACTATCTTATCCCTCCTCACGCTCGGATT 1291

## RESULT 4

US-08-461-018A-2  
; Sequence 2, Application US/08461018A  
; Patent No. 6071694  
; GENERAL INFORMATION:  
; APPLICANT: Akihiko TAKASHIMA et al.  
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WENDEROTH, LIND & PONACK  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
COUNTRY: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,018A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/204,091  
FILING DATE: March 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1972 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: rat  
US-08-461-018A-2

Alignment Scores:  
Pred. No.: 3,82e-236 Length: 1972  
Score: 2015.00 Matches: 386  
Percent Similarity: 98.0% Conservative: 0  
Best Local Similarity: 98.0% Mismatches: 2  
Query Match: 96.8% Indels: 6  
DB: 3 Gaps: 1

US-10-733-816-2 (1-394) x US-08-461-018A-2 (1-1972)

QY 7 GluGlyGlyGly-----MetSerGlyValArgProArgThrThrSerPhe 20  
Db 110 GAAGGAAAGGTGAATCGAAGAGCCATCATGTGGGGCGACCGAGAACCACTCTCTTT 169  
QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40  
Db 170 GCGGAGAGCTGCAAGCCAGTCAGTCAGAGCCCTTCAGCTTTTGTAGCATGAAGTTAGCAGA 229  
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60  
Db 230 GATAAAGATGGCAGCAAGGTAACACACAGTGGTGCAACTCTCTGACAGGGTCTCTGACAGG 289  
QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80  
Db 290 CCACAGGAAGTCAGTTATACACAGACATAAAGTATTGGAAATGGGTCACTTTGGTGTGTA 349  
QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100  
Db 350 TATCAAGCCAACTTTGTGACTCAGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409  
QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120  
Db 410 AAGCGATTTTAAGAACCCAGAGCTCCAGATCATGGAAGCTAGATCACTGTAACTAGTC 469



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Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db 470 CGATTGGCGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTTAACTG 529
Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
Db 530 GTGCTGGACTATGTTCCGGAACAGTGTACAGAGTCCGACAGACTATAGTCGAGCCAG 589
Qy 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
Db 590 CAGACACTCCCTGATGATGTCAAGTTGATATATACAGCTGTTTCAGAACTAGCTAGCC 649
Qy 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
Db 650 TATATCCATTCCTTTGGGATCTGCATCGACATTAACACACACACCTCTTCTGGAT 709
Qy 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
Db 710 CCGTACACAGCTGATTAATACTTCGACTTTGGAAGTGCAGAGCTGTCGAGGA 769
Qy 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGCGCACGAGCTGATCTTTGGA 829
Qy 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
Db 830 GCCACCGATTACAGCTAGTATAGATGTATGGTCTGCAGCGCTGTGTGTGGCTGAATTG 889
Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280
Db 890 TTGCTAGACACACCAATATTTCTTGGGACAGTGTGTGGATCAGTTGGTGGAAATAATA 949
Qy 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300
Db 950 AAGTCTCTAGAACACCAACAGAGGAGCAATATTAGAGAAATGACCCCAATATTACAGAA 1009
Qy 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320
Db 1010 TTCAAAATCCGCCAAATCAAGGACATCTCTTGGACGAAGGTCTTTCCGCCCCGCACTCCA 1069
Qy 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340
Db 1070 CCAGAGGCATTCGACATGTGTAGCCGTCTCTGAGGTACAGCCGACCGCCGCGCTAACCA 1129
Qy 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis 360
Db 1130 CCACTGGAAGCTTGTCACATTCATTTTGTGATGAATTCGGGACCCCAATGTCAAACTA 1189
Qy 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
Db 1190 CCAATGGGCGAGACACACCTGCCCTCTTCAACTTTTACCACCTCAAGAAGCTGTCAAGTAAC 1249
Qy 381 ProProLeuAlaThrIleLeuLeuProProHisAlaArgIle 394
Db 1250 CCACCTCTGGCCACCATCTTATCCCTCTCACGCTCGGATT 1291

RESULT 5
US-09-216-958-2
; Sequence 2, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: Akhiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; DISEASE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
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; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,958
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,018
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; US-09-216-958-2

Alignment Scores:
Pred. No.: 3,82e-236 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: Gaps: 1

US-10-733-816-2 (1-394) x US-09-216-958-2 (1-1972)
Qy 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
Db 110 GAAGGAAGAGTGAATCGAAGAGCCATCATGTGGGGCGACCGAGAACACCTCTTT 169
Qy 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
Db 170 GCGGAGAGCTGCAAGCCAGTCGACAGCCCTTACGCTTTGTAGCATGAAAGTTAGCAGA 229
Qy 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
Db 230 GATAAAGATGCGCAGCAAGGTAAACACAGTGTGGTGGCACTCTCGACAGGGTCTCTGACAGG 289
Qy 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
Db 290 CCACAGGAAGTCAGTTTACACAGACACTAAAGTCAATGGAATGGTCAATTTGGTGTGGTA 349
Qy 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
Db 350 TATCAAGCCAACTTTGTGACTCAGGAGAACTGTGTGGCCATCAAGAAAGTTCTTCAGGAC 409
Qy 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
Db 410 AAGCGATTTAAGAACCCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTC 469
Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db 470 CGATTGGGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTTAACTG 529
Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
Db 530 GTGCTGGACTATGTTCCGGAACAGTGTACAGAGTCCGACAGACTATAGTCGAGCCAG 589
Qy 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
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Db 1216 TTTGGAAGTCAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTGGTATATCTGTTCTCGG 1275  
Qy 231 TTTTyrArgAlaProGluLeuLeuPheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 1276 TACTATAGGACCAAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATA 1335  
Qy 251 TTPSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 1336 TGGTCTGCTGGCTGTGTGGCTGAGCTGTTACTAGGACCAACCAATATTTCCAGGGGAT 1395  
Qy 271 SerGlyValAspGlnLeuValGluIleIleIleValLeuGlyThrProThrArgGluGln 290  
Db 1396 AGTGGTGTGATCAGTTGGTAGAAATAATCAAGTCTCTGGGAATCCCAAGGGAGCAA 1455  
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 1456 ATCAGAGAAATGAACCCAACTACACAGATTTAAATTCCTCAATTAAGGCACATCT 1515  
Qy 311 TTPThrIysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330  
Db 1516 TGGACTAAGGCTCTCCGACCCGAACTCCACCGAGGCAATTCACCTGTGTAGCCGCTG 1575  
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 1576 CTGGAGTATACCACTGCTCCGACTAACCACTGGAAGCTTGTGCACATTCATTTTT 1635  
Qy 351 AspGluLeuArgAspProAsnValIysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1636 GATGAATACGGGACCCAAATGTCNAACTACCAATGGGGGAGACACCTGTCACCTTC 1695  
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuProPro 390  
Db 1696 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCT 1755  
Qy 391 HisAlaArgIle 394  
Db 1756 CATGCTCGGATT 1767

RESULT 7  
US-08-461-018A-1  
; Sequence 1, Application US/08461018A  
; Patent No. 6071694  
; GENERAL INFORMATION:  
; APPLICANT: Akhiko TAKASHIMA et al.  
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: WENDEROOTH, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,018A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/204,091  
; FILING DATE: March 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:

TELEFAX:  
TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2088 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to genomic RNA  
; ORIGINAL SOURCE:  
; ORGANISM: human being  
; US-08-461-018A-1  
Alignment Scores: 1.73e-235 Length: 2088  
Pred. No.: 2010.00 Matches: 382  
Score: 99.7% Conservative: 1  
Percent Similarity: 99.5% Mismatches: 1  
Best Local Similarity: 96.6% Indels: 0  
Query Match: 3 Gaps: 0  
DB:  
US-10-733-816-2 (1-394) x US-08-461-018A-1 (1-2088)  
Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
Db 616 ATGTCAAGGCGGCCAGAACCCCTCTTTCCGAGAGCTGCAAGCCGGTGCAGACGCT 675  
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 676 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGACAGCGCAGCAAGGTGACACAGTG 735  
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
Db 736 GTGCAACTCTCTGGGAGGCTCCAGACAGCGCCACAAGAAATCAGCTATACAGACACTAA 795  
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
Db 796 CTCATTGGAAATGGATCATTTGGTGGGTATATCAAGCCCAACTTTGTGATTGAGGAA 855  
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 856 CTGGTCCCATCAAGAAAGTATTGCGAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC 915  
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 916 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTCGGTATTATTTCTTACTCAGTGT 975  
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 976 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGAAACAGTATAC 1035  
Qy 151 ArgValAlaAArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 1036 AGAGTTGCCAGACACTATAGTCAGGCCAACACAGACGCTCCCTGCTGATTATGTCAGT 1095  
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
Db 1096 TATATGATCAGCTGTTCCGAGTTAGCTATATCCATTCCTTTGGAAATCTGCCATCGG 1155  
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 1156 GATATTAAACCCGAGAACTCTTTGTTGGATCTCTGATACCTGCTATATAAACTCTGTGAC 1215  
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 1216 TTTGGAGTGCAGAGCAGCTGGTCCGAGGAGAACCCCAAGTTTCGTATATCTGTTCTCG 1275  
Qy 231 TTTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 1276 TACTATAGGACCAAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATA 1335  
Qy 251 TTPSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270

Db 1336 TGGTCTGCTGGCTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 1395  
Qy 271 SerGlyValAspGlnLeuValGluLeuValGluLeuValGluLeuValGluLeuValGluLeu 290  
Db 1396 AGTGGTGTGGATCAGTTGGTAGAAATTAATCAAGTCTCTGGGAACTCCCAACAGGGAGCAA 1455  
Qy 291 IleArgGluMetAsnProAsnThrThrGluPheGlyPheProGlnIleValAlaHisPro 310  
Db 1456 ATCAGAGAAATGAACCCAACTACACAGAAATTAATATTCCTCAATTAAGGACATCCT 1515  
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCySerArgLeu 330  
Db 1516 TGGACTAAGTCTTCCGACCCCGAATCTCCACCGGAGGCAATTCACCTGTGTAGCCGCTG 1575  
Qy 331 LeuGluThrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 1576 CTGGAGTATACACCACTGCCCGACTAACCACTGGAAGCTTGTGCACATTCATTTT 1635  
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1636 GATGAATTTAGGGGACCCAAATGTCAAACCTACCAATGGGGAGACACACCTGCACTTTC 1695  
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390  
Db 1696 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCCT 1755  
Qy 391 HisAlaArgIle 394  
Db 1756 CATGCTCGGATT 1767

## RESULT 8

US-09-216-958-1  
; Sequence 1, Application US/09216958  
; Patent No. 6248559  
; GENERAL INFORMATION:  
; APPLICANT: Akihiko TAKASHIMA et al.  
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/216,958  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/461,018  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2088 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to genomic RNA

; ORIGINAL SOURCE:  
; ORGANISM: human being  
US-09-216-958-1

Alignment Scores: 1.73e-235 Length: 2088  
Pred. No.: 2010.00 Matches: 382  
Score: 99.7% Conservativity: 1  
Percent Similarity: 99.5% Mismatches: 1  
Best Local Similarity: 96.6% Indels: 0  
Query Match: 3 Gaps: 0  
DB: 3  
US-10-733-816-2 (1-394) x US-09-216-958-1 (1-2088)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
Db 616 ATGTCAGGGCGGCCAGAACCCACCTCTCTTTCGCGAGAGCTGCAAGCGGTGCAGACGCT 675  
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 676 TCAGCTTTTGGCAGCATGAAGATTAGCAGACAGGACCGCAGCAAGGTGACACAGTG 735  
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
Db 736 GTGGCAACTCTCTGGCGAGGTCCTCCAGACAGGCCACCAAGAGTCAGCTATACAGACACTAA 795  
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
Db 796 CTCATTGGAAATGGATCATTTGGTGGTATATATCAAGCCAACTTTGTGATTCAGGAGAA 855  
Qy 91 LeuValAlaIleLysValLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 856 CTGGTCGCCATCAAGAAAGATTTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 915  
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 916 ATCAGAAAGCTAGATCCTGTAACATAGTCCGATTGCGTTATTTCTTACTCCAGTGT 975  
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 976 GAGAAGAAGATGAGGTCTATCTTAATCTGGTCTGAGCTATGTTCCGGAACAGTATAC 1035  
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 1036 AGAGTTGCCACACACTATAGTCAGGCCAACAGACGCTCCCTGTGATTATATGCAAGTTG 1095  
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyLysCysHisArg 190  
Db 1096 TATATGATCAGCTGTTCCGAAGTTTAGCTATATCATTCCTTTGGAAATCTGCCATCGG 1155  
Qy 191 AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 1156 GATATTAAACCCGAGAACCTCTTGTGGATCTCTGATACCTGCTGTATTTAAACACTCTGTGAC 1215  
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 1216 TTTGGGAAGTGCAGAGCAGCTGTCGAGGGAACCAATGTTTCGTATATCTGTTCTCGG 1275  
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 1276 TACTATAGGGCACACAGATTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 1335  
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 1336 TGGTCTGCTGGCTGTGTGGCTGAGCTCTTACTAGGACCAACCAATATTTTCAGGGGAT 1395  
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
Db 1396 AGTGGTGTGGATCAGTTGGTAGAAATTAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA 1455  
Qy 291 IleArgGluMetAsnProAsnThrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 1456 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAATTAAGGACATCCT 1515

QY 311 TrpThrLysValPheArgProArgThrProProGluAlaLleAlaLeuCysSerArgLeu 330  
 DB 1516 TGGACTAAGGCTCTCCGACCCCGAACTCCACCGAGGCAATTGCACTGTGTAGCGCTG 1575  
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
 DB 1576 CTGGAGTATACCAACTGCGCCGACTAACCACTGGAAGCTTGTGGACATTCATTATTTT 1635  
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
 DB 1636 GATGAATTACGGGACCCCAATGTCAAACTACCAATGGGCGAGACACACCTGCCTCTTC 1695  
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrLleLeuLleProPro 390  
 DB 1696 AACTTCACCACTCAAGAAGTGTCAAGTAATCCACTCTGGCTACCATCTTATTCCTCT 1755  
 QY 391 HisAlaArgTle 394  
 DB 1756 CATGCTCGGATT 1767

RESULT 9  
 US-09-566-921-24  
 ; Sequence 24, Application US/09566921  
 ; Patent No. 668288  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loring, Jeanne F.  
 ; APPLICANT: Tingley, Debora W.  
 ; APPLICANT: Edwards, Carla M.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE  
 ; FILE REFERENCE: PA-0024 US  
 ; CURRENT APPLICATION NUMBER: US/09/566, 921  
 ; CURRENT FILING DATE: 2000-05-05  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 24  
 ; LENGTH: 1952  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. 6682888 234735.15  
 US-09-566-921-24

Alignment Scores:  
 Pred. No.: 2, 15e-186 Length: 1952  
 Score: 1609.00 Matches: 312  
 Percent Similarity: 86.8% Conservative: 24  
 Best Local Similarity: 80.6% Mismatches: 37  
 Query Match: 77.3% Indels: 14  
 DB: 3 Gaps: 3

US-10-733-816-2 (1-394) x US-09-566-921-24 (1-1952)

QY 8 GlyGlyMetSerGlyArgProArgThr---ThrSerPheAlaGluSerCysLysPro 26  
 DB 107 GCGGAGGAGGAGCGGAGGCGCCGCGGAGGCACTAGCTTCCGCGCGCC----- 157  
 QY 27 ValGlnGlnProSerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLys 46  
 DB 158 -----GGGGTGAAGCTGGGCGCT-----GACAGCGGGAAG 187  
 QY 47 ValThrThrValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyr 66  
 DB 188 GTGACACAGTCTGTAGCCACTCTAGGCCAAGGCCGAGCGCTCCCAAGAAGTGGCTTAC 247  
 QY 67 ThrAspThrLysValLleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCys 86  
 DB 248 ACGGACATCAAGTATGGCAATGGCTCATTTGGGTCGTGTACCAAGGACGCGCTGGCA 307  
 QY 87 AspSerGlyGluValAlaLleLysValLeuGlnAspLysArgPheLysAsnArg 106  
 DB 308 GAGACCGGGAAGTAGTCCGCATCAAGAAGGTTCTCCAGGACCAAGAGGTTCAAGAAGCCGA 367

QY 107 GluLeuGlnLleMetArgLysLeuAspHisCysAsnLleValArgLeuArgTyrPhePhe 126  
 DB 368 GAGCTCAGATCATGCTAAGCTGGACCACTGCAATATTGTGAGGCTGAGATATTTC 427  
 QY 127 TyrSerSerGlyGlyLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPro 146  
 DB 428 TACTCCAGTGGCGAGGAAGAAGACGAGCTTTACCTAAATCTGGTGTGGATATGTGCC 487  
 QY 147 GluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValLle 166  
 DB 488 GAGACAGTGTACCGGCTGGCCGCACTTCAACCAAGGCCAAGTTGACCATCCCTATCCTC 547  
 QY 167 TyrValLysLeuLleTyrMetTyrGlnLeuPheArgSerLeuAlaTyrLleHisSerPheGly 186  
 DB 548 TATGTCAAGGTGTACATGTATCCAGCTCTTCCGAGCTTGGCTGAGCCCTACATCCATCC 607  
 QY 187 IleCysHisArgAspLleLysProGlnAsnLeuLeuLeuLeuLeuLeuLeuValLeu 206  
 DB 608 GTGTGTACCGCAGCATCAAGCCCAAGAACCTGCTGTGGAGCCCTGACACTGTGTCTCTC 667  
 QY 207 LysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyr 226  
 DB 668 AAGCTCTGCGATTGTCAGTGCAGAGCAGTTGGTCCGAGGGGAGCCCAATGTCTCTCTAC 727  
 QY 227 IleCysSerArgTyrTyrArgAlaProGluLeuLlePheGlyAlaThrAspTyrThrSer 246  
 DB 728 ATCTGTCTCGCTACTACCGGCGCCAGAGCTCATCTTTGGAGCCCACTGATTACACTCA 787  
 QY 247 SerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProLle 266  
 DB 788 TCCATCGATGTTGGTCAGCTGGCTGTGTACTGGCAGAGCTCTCTTGGGCGAGCCCAIC 847  
 QY 267 PheProGlyAspSerGlyValAspGlnLeuValGluLleLysValLeuGlyThrPro 286  
 DB 848 TTCCCTGGGAGCAGTGGGTGGACAGCTGGTGGAGATCATCAAGGTGCTGGGAACACCA 907  
 QY 287 ThrArgGluGlnLleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnLle 306  
 DB 908 ACCCGGAACAAATCCGAGAGATGAACCCCACTACACGAGTTCAGTTCCCTCAGATT 967  
 QY 307 LysAlaHisProTrpThrLysValPheArgProArgThrProGluAlaLleAlaLeu 326  
 DB 968 AAGCTCACCCCTGGCAAAAGGTGTTCAATCTCGAACCAGCCGAGAGCCATCGCGCTC 1027  
 QY 327 CysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAla 346  
 DB 1028 TGCTTAGCTGTGTGGAGTACACCCCATCTCAAGGCTCTCCCACTAGAGGCTGTGGCG 1087  
 QY 347 HisSerPheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThr 366  
 DB 1088 CACAGCTTCTTTGATGAAGTGGCATGCTGGGAACCCAGCTGCTAACCAACCCCACTT 1147  
 QY 367 ProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrLle 386  
 DB 1148 CCCCCTCTTCAACTTCAGTGTGTGTGAATCTCCATCCACCGTCTCTCTCAAGGCCATT 1207  
 QY 387 LeuLleProProHisAlaArg 393  
 DB 1208 CTCATCCCTCTCTCTTGGAG 1228

RESULT 10  
 US-09-488-856A-3  
 ; Sequence 3, Application US/09488856A  
 ; Patent No. 6316259  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Robert McKay  
 ; APPLICANT: Madeline M. Butler  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP  
 ; FILE REFERENCE: RFS-0115  
 ; CURRENT APPLICATION NUMBER: US/09/488, 856A

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; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)...(1543)
US-09-488-856A-3

Alignment Scores:
Pred. No.: 2,54e-186 Length: 2154
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: Gaps: 4

US-10-733-816-2 (1-394) x US-09-488-856A-3 (1-2154)
Qy 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db 107 CCTCGGGAGCGGCCCTCGGGGCTCGGCAGCGCGGACTAGCTGTTTCGGGAG--- 163
Qy 24 CysLysPro-----ValGlnGln 29
Db 164 -----CCCGCGCGCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 217
Qy 30 ProSerAlaPheGlySerMetLys----- 37
Db 218 CCAGCGCGGACCGCGCGCGGAGGAGGATCTGTCTGGGGCCATGGTGGGGCGCTCGGGGCC 277
Qy 37 ----- 37
Db 278 TCGAGCTCCGGGGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 337
Qy 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 338 GGCACCTAGCTTCCCGCGCGCGCGGGGTGAAGCTGGCGCTGACACGCGGGAAGGTGACACA 397
Qy 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThr 69
Db 398 GTCTGACCACTCTAGGCCAAGGCCCGCAGCGCTCCCAAGAGTGGCTTACACGGACATC 457
Qy 70 LysValIleGlyAanGlySerPheGlyValValFyrGlnAlaLysLeuCysAspSerGly 89
Db 458 AAGTGATTGGCAATGGCTCATTTGGGGTCTGTGTACCGAGCAGCGCTGGCAGACACGAG 517
Qy 90 GluLeuValAlaLleLysLysValLeuGlnAspLysArgPheLysAanArgGluLeuGln 109
Db 518 GAACCTAGTCGCATCAAGAGGTTCTCCAGGACAAAGAGTTCAAGAACCGAGAGCTCAG 577
Qy 110 IleMetArgLysLeuAspHisCysAanIleValArgLeuArgTyrPhePheTyrSerSer 129
Db 578 ATCATGGTATAGCTGGACCACTGCATATTTGTAGGCTGAGATCTTTTCTACTCCAGT 637
Qy 130 GlyLysLysLysAspGluValTyrLeuAanLeuValLeuAspTyrValProGluThrVal 149
Db 638 GGCAGAGAAGAACGAGCTTACTTAATCTGGTGTGGAATATGTGCCCGAGACAGTG 697
Qy 150 TyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 698 TACCGGGTGGCGCCCACTTCCACAGCCCAAGTTGACCATCCCTATCTCTATGTCAAG 757
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyLysCysHis 189
Db 758 GTGTACATGTACCAAGCTCTTCCGAGGCTTGGCTTACATCCATCCCGAGGGCGGTGTCTAC 817
Qy 190 ArgAspLysProGlnAanLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 209
Db 818 CGCGACATCAAGCCCGAGAACCTGTGTGGAGCCCTGACACTGTGTCTCAAGCTCTGC 877

RESULT 11
US-09-578-194-6
; Sequence 6, Application US/09578194
; Patent No. 6822139
; GENERAL INFORMATION:
; APPLICANT: Sudwestdeutsche Saat-zucht-SWS
; APPLICANT: Advanta Seeds B.V.
; TITLE OF INVENTION: Modulation of Storage Organs
; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/09/578,194
; CURRENT FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(1636)
; OTHER INFORMATION: strain Columbia ecotype
; OTHER INFORMATION: taxon:3702
; OTHER INFORMATION: tissue type leaves
; OTHER INFORMATION: clone lib lambda ZAPII
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lechamy, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SGS/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
; TITLE: from Arabidopsis thaliana ( Accession No. 6822139 X94938, x94939 and X99696)
; TITLE: (008)
; JOURNAL: Plant Physiol.
; VOLUME: 113
; ISSUE: 1
; PAGES: 306-306
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Db      879  GTGGACGAGCTAGTGAGGATCATAAAGGTTCTTTGGTACTCCAATCGCGAAGAAATCCCG 938
Qy      293  GluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyrThr 312
Db      939  TGCATGAACCAACTACAGAGATTCCAGATTCACACAAATCAAGACCCACCCTTGGCAT 998
Qy      313  LysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeuLeuGlu 332
Db      999  AAGGTTTCCACAAAGCGGATGCCCTCGGGAAGCCATTGACCTTCGCATCTCGGCTTCTTCAA 1058
Qy      333  TyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePheAspGlu 352
Db      1059  TACTCACCAGTCTAGCTTGCATTCGCCTCGAGCATGTGGCATCCGTTTTTCAATGAA 1118
Qy      353  LeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsnPhe 372
Db      1119  CTCGGTGAGCAAAATGCTCGTCTCTCCAAATGGCGGACCTTACCACCGTTGTTCAACTTC 1178
Qy      373  ThrThrGlnGluLeuSer---SerAsnProProLeuAlaThrIleLeuIleProProHis 391
Db      1179  ---AAACAAGAGTTGTCTGGGGCTTCCCGGAGCTTATCAACAGGCTTAATACCAGAGCAT 1235
Qy      392  AlaArg 393
Db      1236  GTGAGG 1241

RESULT 12
US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-347-801-9

Alignment Scores:
Pred. No.:      8.94e-142      Length:      1814
Score:          1244.50      Matches:      246
Percent Similarity: 73.2%      Conservative: 54
Best Local Similarity: 60.0%      Mismatches:  90
Query Match:      59.8%      Indels:      20
DB:               3          Gaps:         5

US-10-733-816-2 (1-394) x US-09-347-801-9 (1-1814)
Qy      3  TyrMetProMetClnGlyGlyGlyMetSerGlyArg-ProArgThrThr----- 18
Db      212  TATATAGCTCTGTCGAGCATGGCCCTCGGTGGCGTGGCAGCGCTCTCTTTGGGATTTCA 271
Qy      19  ---SerPheAlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLys 37
Db      272  GAATGGCACAAGTTCTAGCAGTGCACCCAGATCGTCTTCCACAGAGTTGGCAGTATGAG 331
Qy      37  sValSerArgAspLysAspGlySerLysValThrThr----- 49
Db      332  CATAAGGGACGACAAGGACGTTGAAGATATTGTAGTCAATGGCAATGGGCGGAGCGCTGG 391
Qy      50  -----ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTy 66
Db      392  TCATATCATAGTCACGAGCATTTGATGGGAGAAATGGCGAGGCAAGCAGACCATTAGTTA 451

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QY 66 rThrAspThrLysValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCy 86
Db 452 CATGGCTGAGCGGTGGTGGTCTCGGAAACCGTTTCCAGGCCAAGTGTCT 511
QY 86 sAspSerGlyGluLeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnAr 106
Db 512 TGAACCTGGTGAGACCGTCTATATAAAGGTTCTTCAAGACAGAGATACAAGATCG 571
QY 106 gGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePh 126
Db 572 TGAGCTGCAAAACCATCGAGTCTTGACCAACCAATGTGGTGGCTTAAAGCACTGTTT 631
QY 126 eTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPr 146
Db 632 CTTCTCAAAGACTGAG---AAAGAGGAGCTTTACCTCAATTTGGTGTGATGTATGACC 688
QY 146 oGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValI 166
Db 689 GGAGACTGCTCATCGTGTCTAAACATTAACAAGATGAACAGCGCATGCTTTGAT 748
QY 166 eTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHis---SerPh 185
Db 749 TTATGCAAAACTGTATATGATGATCAGATTTGTAGAGCCTTGGCATACATTCAACAACGAT 808
QY 185 eGlyIleCysHieArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaVa 205
Db 809 TGGAGTGTGCCACAGGACATTAAAGCGCAAAATCTCTCTGTTAATCTCTATATCCATCA 868
QY 205 lLeuLysLeuCyAspPheGlySerAlaLysGlnLeuValArgGluProAsnValSe 225
Db 869 GCTAAAAATTGTGACTTTGGCAGCGGAAAGTTCTGTGTAAAGCGCAACCAATTC 928
QY 225 rTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrTh 245
Db 929 TTACATCTGTTCTAGGTACTACAGAGCTCCAGAGCTCATATTGGTGTCTCAATACAC 988
QY 245 rSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlnPr 265
Db 989 AACAGCCATTGATGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1048
QY 265 oIlePheProGlyAspSerGlyValAspGlnLeuValGluIleLysValLeuGlyTh 285
Db 1049 TCGTTCCTTGGAGAAAGCGGTGTTGATCAGCTTTGTAATCATCAAGGTTCTGGGCAC 1108
QY 285 rProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGl 305
Db 1109 ACCACACGCTGAGAAATTAAGTGTCAATGAATCCAAATTAATACCGAGTTTAAATCCGCA 1168
QY 305 nIleLysAlaHisProTrpThrLysValPheArgProArgThrProGluAlaIleAl 325
Db 1169 AATCAAAAGCTCACCATGGCATTAAGATATTCCATAAAGAGATGCTGCTGAAGCGGTAGA 1228
QY 325 aLeuCySerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCy 345
Db 1229 TCTGTTCCAGGTTCTGAGTACTCACCAAACTTCAGTCTGCTGCTGCTGCTGCTGCTGCTG 1288
QY 345 sAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAs 365
Db 1289 GGTCCATCCGTTCTTGTATGAACCTTCGGGATCCAAACACCGCTTACCGAATGGTCTGTT 1348
QY 365 pThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnPro---ProLeuAl 384
Db 1349 TCTTCCGCTCTCTTCAATTTTAAAGCCCATAGAGCTGAAGAAACGTGCCGCGGATTTTCAT 1408
QY 384 aThrIleLeuIleProProHisAlaArg 393
Db 1409 GGTGAATTTGGTCTCTGAGCATGACCG 1436
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RESULT 13

US-09-854-731-9

; Sequence 9, Application US/09854731

; Patent No. 6794561

## GENERAL INFORMATION:

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; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-854-731-9
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## Alignment Scores:

Pred. No.:	8 94e-142	Length:	1814
Score:	1244.50	Matches:	246
Percent Similarity:	73.2%	Conservative:	54
Best Local Similarity:	60.0%	Mismatches:	90
Query Match:	59.8%	Indels:	20
DB:	3	Gaps:	5

US-10-733-816-2 (1-394) x US-09-854-731-9 (1-1814)

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QY 3 TyrMetProMetGluGlyGlyMetSerGlyArg-ProArgThrThr----- 18
Db 212 TATATAGCTCTGTCCGACGATGGCTCGGTGGCGTGGCAGCGCTCTCTTTGGGATTCA 271
QY 19 ----SerPheAlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLys 37
Db 272 GAATGSCACAAGTCTTAGCAGTGACCCAGATCGTCTTCCCAACGAGTGTGGCGATATGAG 331
QY 37 sValSerArgAspLysAspGlySerLysValThr----- 49
Db 332 CATAAAGGACGACAGGACGTTGAAGATATTGTAGTCAATGGCAATGGGGCGGAGCTGG 391
QY 50 -----ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTy 66
Db 392 TCATATCATAGTGACCGACATTTGATGGAGAAATGGCGAGCAAGCAAGCAGCATTAAGTTA 451
QY 66 rThrAspThrLysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCy 86
Db 452 CATGGCTGAGCGGTGGTGGTCTTGGAAACCGTTTCCAGGCCAAGTGTCT 511
QY 86 sAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnAr 106
Db 512 TGAACCTGGTGAGACCGTACTATATAAAGGTTCTTCAAGACAGAGATACAAGATCG 571
QY 106 gGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePh 126
Db 572 TGAGCTGCAAAACCATCGAGTCTTGACCAACCAATGTGGTGGCTCTTAAAGCACTGTTT 631
QY 126 eTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPr 146
Db 632 CTTCTCAAAGACTGAG---AAAGAGGAGCTTTACCTCAATTTGGTGTGATGTATGACC 688
QY 146 oGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValI 166
Db 689 GGAGACTGCTCATCGTGTCTAAACATTAACAAGATGAACAGCGCATGCTTTGAT 748
QY 166 eTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHis---SerPh 185
Db 749 TTATGCAAAACTGTATATGATGATCAGATTTGTAGAGCCTTGGCATACATTCAACAACGAT 808
QY 185 eGlyIleCysHieArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaVa 205
Db 809 TGGAGTGTGCCACAGGACATTAAAGCGCAAAATCTCTCTGTTAATCTCTATATCCATCA 868
QY 205 lLeuLysLeuCyAspPheGlySerAlaLysGlnLeuValArgGluProAsnValSe 225
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Db      869  GCTAAATTTGTGACATTTGGCAGCGCGAAAGTTCTGGTAAAGCGCAACCAACATTTC 928
Qy      225  rTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrTh 245
Db      929  TTACATCTGTTCTAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGTACTGTAATACAC 988
Qy      245  rSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnPr 265
Db      989  AACAGCCATTGATGTTGGGTCTGCTGCTGTGTCTGCTGAGCTGCTTCTAGGACAGCC 1048
Qy      265  oIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyTh 285
Db      1049  TCTGTTCCCTGGAGAAAGCGGTGTGATCAGCTGTTGTAATCATCAAGGTTCTGGGCAC 1108
Qy      285  rProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProG1 305
Db      1109  ACCCACAGCTGAAGAAATTAAGTGCATGAATCCAAATTAACCGAGTTAAATTCGCCGA 1168
Qy      305  nIleLysAlaHisProThrLysValPheArgProArgThrProProGluAlaIleAl 325
Db      1169  AATCAAGCTCACCCATGGCATATGATATTCCTAAAGAGATGCTGCTGAAGCGGTAGA 1228
Qy      325  aLeuCysSerArgLeuLeuGluTyrThrProThrAlaAlaArgLeuThrProLeuGluAlaCy 345
Db      1229  TCTGCTGCTCAGGCTTCTGAGTACTACCAAACTTCGGTCTGCTGCTTTGGAGCATT 1288
Qy      345  sAlaHisSerPhePheAspGluLeuArgAspProAsnValIleHisProAsnGlyArgAs 365
Db      1289  GGTCCATCCGTTCTTTGATGAACCTTCGGGATCCAAACACCCGCTTACCGAATGGTCGTT 1348
Qy      365  pThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnPro---ProLeuAl 384
Db      1349  TCTTCGCGCTCTCTTCAATTTTAAGCCCAAGTGAAGTGAAGACGTCGCCGCGGATTTCAT 1408
Qy      384  aThrIleLeuIleProProHisAlaArg 393
Db      1409  GGTGAATTTGGTCCCTGAGCATGCACGG 1436

RESULT 14
US-09-347-801-15      Application US/09347801
; Sequence 15, Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-347-801-15

Alignment Scores:
Pred. No.:      2,78e-141      Length:      1673
Score:          1240.00      Matches:      232
Percent Similarity: 78.6%      Conservative: 65
Best Local Similarity: 61.4%      Mismatches: 69
Query Match:      59.6%      Indels:      12
DB:              3          Gaps:         5

US-10-733-816-2 (1-394) x US-09-347-801-15 (1-1673)

Qy      21  AlaGluSerCysLysProValGlnGln-----ProSerAlaPheGlySerMet 36
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Db      101  GCAGTCGCCCTGCGAGAAAGCAGCAGATGGCGAGCGCGTATGCGAGGGGAAACGAC 160
Qy      37  LysValSerArgAspLysAspGlySerLysValThrThrValValAlaIleThrProGlyGln 56
Db      161  GCCATGACC-----GGTCACATCATCTCCACACCACCATCGCC-----GSCAAG 202
Qy      57  GlyProAspArgProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySer 76
Db      203  AACGGCGAGGCCAACGACGATAGCTACATGCGCGAGCGCGTGTGTGGCATTGGTTTCG 262
Qy      77  PheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLys 96
Db      263  TTTGGCATCTCTTTACGGCTAAATGCTCGTGAACCGGGAGATGGTGGGCATTAAAGAG 322
Qy      97  ValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHis 116
Db      323  GTACTGCAGCAGCAGCGTACAGACCGTGCAGCTGATGCTTATCGCTTCGATGATCCAT 382
Qy      117  CysAsnIleValArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluVal 136
Db      383  TCCAATGTTGTTCTCCCTCAAGCACTGCTTCTTCTCAACC---ACAAGTAGAGATGAGCTG 439
Qy      137  TyrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArgValAlaIleArgHisTyr 156
Db      440  TTCTTGAACTTGTATGGAGTATGTCGCGAGACGCTATACCGCGTGTCTTAAGCATCTAC 499
Qy      157  SerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPhe 176
Db      500  AGTAATGCCAACCAACGAGGATGCGCTTATCTATGTCAAGCTTTACATGATCAGCTTTT 559
Qy      177  ArgSerLeuAlaTyrIleHisSerPhe---GlyIleCysHisArgAspIleLysProGln 195
Db      560  AGAGGGCTAGCTTATGTTTCTACTGTTCCAGGAGTTTGGCCACAGGAGTGTGAACACCAA 619
Qy      196  AsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLys 215
Db      620  AATGTTTGTGTTGATCTCTTAACCCATCAAGTCAAGATCTGTGACTTTTGAAGTGCANAA 679
Qy      216  GlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaPro 235
Db      680  GTTCTGTGCTGCTGGTGAACCAACACATAGCATATATGCTCTCGCTACTATCGTCTCT 739
Qy      236  GluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCys 255
Db      740  GAGCTCATATTTGGTGCAACTGAATATACAACTTCAATAGACATATGCTCAGCTGGATGT 799
Qy      256  ValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGln 275
Db      800  GTTCTTTCAGAGAGCTACTTCTTGTGTCAGCTCTGTTTCCAGGAGAGACTGCGGTGTGATCAG 859
Qy      276  LeuValGluIleLysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsn 295
Db      860  CTAGTGGAGATATCAAGGTTCTTGGTACTCCAAACCGTGAAGAAATTCGGTGCATGAC 919
Qy      296  ProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProThrThrLysValPhe 315
Db      920  CCCAACTATACCGAGTTCAGGTTTCTCAGATTAAAGGCTCATCTCTGGCACAAGATTTC 979
Qy      316  ArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrPro 335
Db      980  CACAAGAGAAATGCCCGCTGAAGCTATAGATCTTGGCTCCCGCTCTCTCCAGTATTACCA 1039
Qy      336  ThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAsp 355
Db      1040  AATCTAGTGTGCACTGCTCTTGTATGATGTGTCATCTCTTCTTGTATGATGACTACGTGAG 1099
Qy      356  ProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGln 375
Db      1100  CCGAATGCACGCTTGGCGAATGGCGCCCATTCCTCTCTGTTCAACTTCAAACTGAA 1159
Qy      376  GluLeuSerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArg 393
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US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURES:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-854-731-15
Alignment Scores:
Pred. No.: 2,78e-141 Length: 1673
Score: 1240.00 Matches: 232
Percent Similarity: 78.6% Conservative: 65
Best Local Similarity: 61.4% Mismatches: 69
Query Match: 59.6% Indels: 12
DB: 3 Gaps: 5
US-10-733-816-2 (1-394) x US-09-854-731-15 (1-1673)
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Db 101 GCAGTGCCTCGCGAAGAACAGCAGGATGGCGAGCGCGGTATGCGGAGGGGAACGAC 160
QY 37 LysValSerArgAspLysAspGlySerLysValThrThrValValAlaThrProGlyGln 56
Db 161 GCCATGACC-----GGTCACATCATCTCCACCACCACCATCGGC-----GGCAAG 202
QY 57 GlyProAspArgProGlnGluValSerTyThrAspThrLysValIleGlyAsnGlySer 76
Db 203 AACGGCGAGCCCAAGCAGCAGATAGCTACATGCGGAGCGCGTGTGGCACTGGTTCG 262
QY 77 PheGlyValValTyrglnAlaLysLeuLysCysAspSerGlyGluLeuValAlaLysLys 96
Db 263 TTTGGCATCGTCTTTCAGGCTAAATGCTCGAACCAGGAGATGGTGGCATTTAGAAAG 322
QY 97 ValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHis 116
Db 323 GTACTGCAGCAGCAGCGTACAGAACCGTGAGTGCAGTCTTATGCTTCGATGATCCAT 382
QY 117 CysAsnIleValArgLeuArgTyrrPhePheTyrrSerSerGlyGluLysLysAspGluVal 136
Db 383 TCCAAATGTTCTCTCCCTCAAGCAGCTGCTTCTTCTCAACC---ACAAGTAGAGATGAGCTG 439
QY 137 TyrrLeuAsnLeuValLeuAspTyrrValProGluThrValTyrrArgValAlaArgHisTyrr 156
Db 440 TTCTGTAACTTGTGATGGAGTAGTCTCCGAGACGCTATACCGCGTCTTAAGCAGCTAC 499
QY 157 SerArgAlaLysGlnThrLeuProValIleTyrrValLysLeuTyrrMetTyrrGlnLeuPhe 176
Db 500 AGTAATGCCAACACGAGGGATGCGCTTATCTATGCTCAAGCTTTACATGATCAGCTTTT 559
QY 177 ArgSerLeuAlaTyrrIleHisSerPhe---GlyIleCysHisArgAspIleLysProGln 195
Db 560 AGAGGGCTAGCTTATGTTCTACTGTTTCCAGGAGTTTGGCCACAGGGATGTGAACCCAA 619
QY 196 AsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuLysCysAspPheGlySerAlaLys 215
Db 620 AATGTTTTGGTGTATCTCTAACCCTCAAGTCAAGTCTGTGACTTGTGAAGTGCAGAA 679
QY 216 GlnLeuValArgGlyGluProAsnValSerTyrrIleCysSerArgTyrrTyrrArgAlaPro 235
Db 680 GTTCTGGTACCTGGTGAACCCCAACATAGCATATATGCTCTCGTACTATATCGTCTCT 739
QY 236 GluLeuIlePheGlyAlaThrAspTyrrThrSerSerIleAspValTrpSerAlaGlyCys 255
Db 740 GAGCTCATATTTGGTGAACCTGAATATACAACCTTCAATAGACATATGGTCAGTGTATGT 799
QY 256 ValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGln 275
Db 800 GTTCTTGCAGAGCTACTTCTTGGTCAAGCTCTCTTCCAGGAGAGACTGGCGTTGATCAG 859
QY 276 LeuValGluIleIleLysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsn 295
Db 860 CTAGTGGAGATTATCAAGGTTCTTGGTACTCCAAACCGTGAGGAAATTCGGTGCATGAAC 919
QY 296 ProAsnTyrrThrGluPheLysPheProGlnIleLysAlaHisProThrThrLysValPhe 315
Db 920 CCAACTATACCGAGTTCAGGTTTCTCAGATTAAAGCTCATCTTGGGCAACAGATTTC 979
QY 316 ArgProArgThrProGluAlaIleAlaLeuLysCysSerArgLeuLeuGluTyrrThrPro 335
Db 980 CACAAGAGATGCCCGCTGAGCTATAGATCTTGCCTCCGCGCTTCTCCAGTATTACCA 1039
QY 336 ThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAsp 355
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QY 356 ProAsnValLysHisProGlyArgAspThrProAlaLeuPheAsnPheThrThrGln 375
Db 1100 CCGAATGCAGCTTGCAGATGGCGCCCAATTCCTCTCTGTTCACCTTCAACCTGAA 1159
QY 376 GluLeuSerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArg 393
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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
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10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
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16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Query		
No.	Score	Match Length	ID Description
1	2024	97.3	1389 7 US-10-181-543-3 Sequence 3, Appli

2	2024	97.3	1389	7	US-10-305-720-1414	Sequence 1414, Ap
3	2024	97.3	1389	9	US-10-772-636-71	Sequence 71, Appl
4	2024	97.3	1389	10	US-10-840-060-256	Sequence 256, App
5	2024	97.3	1389	16	US-11-288-493-71	Sequence 71, Appl
6	2015	96.8	1525	16	US-11-004-763-15	Sequence 15, Appl
7	2015	96.8	1972	3	US-09-866-712-2	Sequence 2, Appli
8	2013	96.7	1211	10	US-10-504-173-44	Sequence 44, Appl
9	2013	96.7	1263	9	US-10-482-524-6	Sequence 6, Appli
10	2013	96.7	1389	9	US-10-482-524-3	Sequence 3, Appli
11	2013	96.7	1815	9	US-10-357-930-30285	Sequence 30285, A
12	2012	96.7	1474	16	US-11-004-763-17	Sequence 17, Appl
13	2010	96.6	1503	7	US-10-613-728-7	Sequence 1, Appli
14	2010	96.6	2088	3	US-09-866-712-1	Sequence 1, Appli
15	1996.5	95.9	1639	6	US-10-278-759-13	Sequence 13, Appl
16	1996.5	95.9	1639	8	US-10-302-812-61	Sequence 61, Appl
17	1996.5	95.9	1639	9	US-10-828-669-10	Sequence 10, Appl
18	1996.5	95.9	1639	10	US-10-887-553A-275	Sequence 275, App
19	1996.5	95.9	1639	10	US-10-770-726-21	Sequence 21, Appl
20	1925	92.5	1685	16	US-11-136-527-3081	Sequence 3081, Ap
21	1750.5	84.1	1864	7	US-10-062-674-1877	Sequence 1877, Ap
22	1634.5	78.5	1698	10	US-10-491-467-65	Sequence 5, Appli
23	1609	77.3	1452	9	US-10-482-524-5	Sequence 24, Appl
24	1609	77.3	1952	10	US-10-765-700-24	Sequence 2, Appli
25	1609	77.3	2154	7	US-10-181-875-3	Sequence 11, Appl
26	1609	77.3	2169	6	US-10-278-759-11	Sequence 11, Appl
27	1609	77.3	2169	9	US-10-482-524-1	Sequence 274, App
28	1609	77.3	2169	10	US-10-887-553A-274	Sequence 9, Appli
29	1609	77.3	2170	6	US-10-278-759-9	Sequence 4597, Ap
30	1609	77.3	2374	9	US-10-723-860-4597	Sequence 241, App
31	1607	77.2	2155	10	US-10-486-706-241	Sequence 2430, App
32	1607	77.2	2167	16	US-11-136-527-2430	Sequence 254, App
33	1542.5	74.1	3477	10	US-10-840-060-254	Sequence 4571, Ap
34	1542.5	74.1	3477	13	US-11-097-143-4571	Sequence 2, Appli
35	1294	62.2	1849	7	US-10-292-408-2	Sequence 29872, A
36	1273	61.2	1922	8	US-10-437-963-29872	Sequence 133605, A
37	1262	60.6	2164	8	US-10-424-599-133605	Sequence 36269, A
38	1259.5	60.5	1523	7	US-10-292-408-23	Sequence 31098, A
39	1258.5	60.4	1813	8	US-10-425-114-31098	Sequence 98579, A
40	1257.5	60.4	1831	8	US-10-437-963-98579	Sequence 32039, A
41	1257.5	60.4	1881	8	US-10-425-114-32039	Sequence 49442, A
42	1257.5	60.4	1980	9	US-10-425-115-49442	Sequence 9996, Ap
43	1257.5	60.4	2794	8	US-10-437-963-9996	Sequence 30667, A
44	1254.5	60.3	2794	8	US-10-425-114-30667	
45	1252	60.2	1675	8	US-10-425-114-30667	

ALIGNMENTS

RESULT 1  
US-10-181-543-3  
; Sequence 3, Application US/10181543  
; Publication No. US20030211608A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Madeline M. Butier  
; APPLICANT: Robert McKay  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION  
; FILE REFERENCE: RTSP-0339  
; CURRENT APPLICATION NUMBER: US/10/181,543  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 3  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)...(1302)  
US-10-181-543-3

Alignment Scores:  
Pred. No.: 1,16e-240 Length: 1389  
Score: 2024.00 Matches: 384  
Percent Similarity: 100.0% Conservatives: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.3% Indels: 0  
DB: 7 Gaps: 0

US-10-733-816-2 (1-394) x US-10-181-543-3 (1-1389)

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Db 40 ATGTGAGGGCGCCGAGAACCTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 99  
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGCAAGGACGCGCAGCAACAGTG 159  
Qy 51 ValAlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAGCTATACAGACTAAA 219  
Qy 71 ValileGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
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Qy 91 LeuValAlaLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 280 CTGGTGGCCATCAAGAAGATTGTCAGACAGAGATTTAAGAATCGAGAGCTCCAGATC 339  
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 340 ATGAGAAAGCTAGATCATCTGAATAGTCCGATGGCTGCTATTTCTTCTACTCCAGTGT 399  
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGTGAGCTATGTTCCGGAAACAGTATAC 459  
Qy 151 ArgValAlaAlaHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 460 AGAGTTGCCAGACATATATGTCAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 519  
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
Db 520 TATATGTATCAGCTGTTCCGAAGTTTAGCCCTATATCCATTTCTTTGGAATCTGCCATCGG 579  
Qy 191 AspLysLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 580 GATATTAAACCGCAAGAACCTCTGTGTGATCCTGATCTGCTGTATTTAAACTCTGTGAC 639  
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 640 TTTGGAAGTGCNAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTGGTATATCTGTCTCGG 699  
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 700 TACTATAGGACCACAGAGTTGATCTTTTGGAGCCACTGATTATATACCTCTAGTATAGATGA 759  
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 760 TGGTCTGCTGCTGTGTGTGGCTGAGCTGTATCTAGCAACCACTATTTTCCAGGGAT 819  
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
Db 820 AGTGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTGGGAATCTCCAAAGGAGGACAA 879  
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 880 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTTCCCTCAAAATTAAGAGCACATCCT 939  
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330

940 TGGACTAAGGTCTTCCGAGCCCGAACTCCACCGGAGGCAATTCGACTGTGTAGCGGTCTG 999  
331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
1000 CTGGAGTATACACAACTGCCGACTAACACCACTGGAAGCTTGTGCACATTCATTTTTT 1059  
351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
1060 GATGAATTCAGGAGCCCAATGTCAAACATCCAAATGGGCGAGACACACCTGCACCTTC 1119  
371 AsnPheThrThrGlnGluLeuSerSerAsnProLeuAlaThrIleLeuIleProPro 390  
1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCCT 1179  
391 HisAlaArgIle 394  
1180 CATGCTCGGATT 1191

RESULT 2  
US-10-305-720-1414  
; Sequence 1414, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
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; TYPE: DNA  
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; FEATURE:  
; NAME/KEY: misc feature  
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US-10-305-720-1414

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Score: 2024.00 Matches: 384  
Percent Similarity: 100.0% Conservatives: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.3% Indels: 0  
DB: 7 Gaps: 0

US-10-733-816-2 (1-394) x US-10-305-720-1414 (1-1389)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysValProValGlnGlnPro 30  
Db 40 ATGTGAGGGCGCCGAGAACCTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 99  
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGCAAGGACGCGCAGCAACAGTG 159  
Qy 51 ValAlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAGCTATACAGACTAAA 219  
Qy 71 ValileGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
Db 220 GTGATTGGAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCAGGAA 279  
Qy 91 LeuValAlaLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 280 CTGGTGGCCATCAAGAAGATTGTCAGACAGAGATTTAAGAATCGAGAGCTCCAGATC 339  
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 340 ATGAGAAAGCTAGATCATCTGAATAGTCCGATGGCTGCTATTTCTTCTACTCCAGTGT 399



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Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCGGATTGGTTATTTCTTCTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACATATAGTCAGCCAAACAGACGCTCCCTGTGATTTATGTCAGATTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGATACAGCTGTTCCGAGTTAGCCTATATCCATTCCTTGGAACTCGCCATCG 579
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTGTTGGATCCTGATACCTGCTGTATTAAAACTCTGTAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTTGGAAGTCAAGACAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 699
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
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Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
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Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
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Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
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Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGCAATTGCACCTGTGTAGCCGCTG 999
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACACAACTGCCCGACTAACCACTGGAAGCTGTGTGCACATTCATTTT 1059
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1060 GATGATTAACGGACCCCAATGTCAAACATCCAAATGGCGGACACACACCTGCACCTTC 1119
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAAATCCACCTCTGGCTACCATCCTTATTCCTCT 1179
Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191

RESULT 3
US-10-772-636-71
; Sequence 71, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Allen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5991,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
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; TITLE OF INVENTION: 5014
; FILE REFERENCE: MP103-015PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/772,636
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-10-772-636-71

Alignment Scores:
Pred. No.: 1.16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 9 Gaps: 0

US-10-733-816-2 (1-394) x US-10-772-636-71 (1-1389)
Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTCAAGGGCGGCCAGAACCACTCTCTTCCGAGAGCTGCAGCGCGTGCAGCAGCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGCGCAGCAAGGTGACAACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGGCGAGGTCCTCAGACAGGCCCAAGAACTAGCTATACAGACACTAA 219
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTTGGAATGATGATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGATTATTCAGGACAAGAGATTTTAAAGAAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGCTAACTAGTCCGATTCGCTTATTTCTTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATAC 459
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Db 820 AGTGGTGGATCAGTTGGTAGAAATTAATCAAGTCTCGGAACCTCCAAACAGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 880 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
Qy 311 TTPThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGTCTTCCGACCCCGAACCCTCCACCGAGGCAATTCACATGTGTAGCCGCTG 999
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACACCACTGCCCACTAACCACTCAAAATCGGCGAGACACACCTGCACCTTC 1059
Qy 351 AspGluLeuArgPheProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1060 GATGAATACCGGACCCCAATGTCAAAATCCAAATCGGCGAGACACACCTGCACCTTC 1119
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGCTACCATCTTATTCCTCCT 1179
Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191

RESULT 5
US-11-288-493-71
; Sequence 71, Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MP103-015PIRNONMIN
; CURRENT APPLICATION NUMBER: US/11/288,493
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
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; PRIOR APPLICATION NUMBER: US 60/460,279
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; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-11-288-493-71
Alignment Scores:
Pred. No.: 1,16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 16 Gaps: 0

US-10-733-816-2 (1-394) x US-11-288-493-71 (1-1389)
Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTCAAGGCGCGCCAGAACCACTCTCTTTGCGAGAGCTGCAAGCCGGTGACAGCGCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGACAGGACGCGCAGCAAGGTGACAACTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGCTCCAGACAGGCCCAAGAGTCAGCTATACAGACACTAAA 219
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATCGATCACTTTGCTGGTATATCAAGCCAACTTGTGTGATTGAGGAGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGTATTTCGAGGACAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGAACATAGTCCGATTCGATTATTTCTTCTACTCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAAGATCAGGCTCTATCTTAATCTGCTGCTGAGTACTGTTCGGGAAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATAGTCAGGCAACACAGACGCTCCCTGTGATTATGTCAAGTTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGTATCAGCTGTTCGGAAGTTTAGCCTATATCCATTCCTTTGGAAATCTGCCATCGG 579
Qy 191 AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCTGTACTGTCTGTATTAAAACCTCTGTGAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTTGGAAGTCAAAGCAGCTGGTCCGAGGAGAACCAATGTTTCGTATATATCTGTCTCGG 699
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGACACAGAGTTGATCTTTGGAGCCACCTGATTATATACCTCTAGTATAGATGA 759
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTTCCAGGGAT 819
Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGGAACCTCCAAACAGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
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Db 880 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939  
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaAlaLeuCysSerArgLeu 330  
Db 940 TGGACTAAGGTCTTCGACCCGAACTCCACCGAGGCAATTCGACTGTGTAGCCGCTG 999  
Qy 331 LeuGluThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 1000 CTGGAGTATACACAACTGCCCGCACTAACACCACTGGAACTTGTGCACATTCATTTTT 1059  
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1060 GATGAATTACGGGACCCCAATGTCAACATCCAAATCGGGGAGACACACCTGCACCTTC 1119  
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrLeuLeuProPro 390  
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCT 1179  
Qy 391 HisAlaArgile 394  
Db 1180 CATGCTCGGATT 1191

## RESULT 6

US-11-004-762-15  
; Sequence 15 Application US/11004762  
; Publication No. US20060003953A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Joshua Finger  
; APPLICANT: Ravi Jain  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Kathleen Myers  
; TITLE OF INVENTION: Compositions and their uses directed to bone growth modulators  
; FILE REFERENCE: BIOLO050US  
; CURRENT APPLICATION NUMBER: US/11/004,762  
; CURRENT FILING DATE: 2004-12-03  
; PRIOR APPLICATION NUMBER: US 60/527,370  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/527,173  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/527,172  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/527,420  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/527,174  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/527,397  
; PRIOR FILING DATE: 2003-12-04  
; NUMBER OF SEQ ID NOS: 680  
; SOFTWARE: PatentSeq version 1.0  
; SEQ ID NO 15  
; LENGTH: 1525  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-004-762-15

Alignment Scores:  
Pred. No.: 1.79e-239 Length: 1525  
Score: 2015.00 Matches: 386  
Percent Similarity: 98.0% Conservative: 0  
Best Local Similarity: 98.0% Mismatches: 2  
Query Match: 96.8% Indels: 6  
DB: 16 Gaps: 1

US-10-733-816-2 (1-394) x US-11-004-762-15 (1-1525)

Qy 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20  
Db 110 GAAGGAAAGGTGAATCGAGAGAGCCATCATGTGCGGGGCGACCGAGAACCACTCTCTTT 169

Qy 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40  
Db 170 GCGGAGAGCTGCAGCCAGCAGCTTCAGCTTTTGGTAGCATGAAGATTAGCAGA 229  
Qy 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60  
Db 230 GATTAAGATGGCAGCAAGGTAAACACAGTGGTGGCACTCTCTGGACAGGGTCTTGACAGG 289  
Qy 61 ProGlnGluValSerTyrThrAspThrLysValLleGlyAsnGlySerPheGlyValVal 80  
Db 290 CCACAGGAAGTCAAGTTACACAGACACTAAAGTCATTGGAAATCGGTCAATTTGGTGTGTA 349  
Qy 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaLleLysLysValLeuGlnAsp 100  
Db 350 TATCAAGCAAACTTTGTGACTCAGAGAACTGGTGGCCATCAAGAAAGTTCTTCAGGAC 409  
Qy 101 LysArgPheLysAsnArgGluLeuGlnLleMetArgLysLeuAspHisCysAsnLleVal 120  
Db 410 AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTC 469  
Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140  
Db 470 CGATTGCGGTATTTCTTCTACTCGAGTGGCGAGAAAGATCAGGTCTACCTTAACCTG 529  
Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160  
Db 530 GTGCTGGACTATGTTCCGAAACAGTGTACAGAGTCGCCAGACACTATATAGTCAGGCAAG 589  
Qy 161 GlnThrLeuProValLleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180  
Db 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACCAGCTGTTCAAGTCTAGCC 649  
Qy 181 TyrIleHisSerPheGlyLleCysHisArgAspLleLysProGlnAsnLeuLeuAsp 200  
Db 650 TATATCCATTCCTTTGGGACTCTGCCATCGAGACATTAACCCACAGAACCTCTTGCTGGAT 709  
Qy 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220  
Db 710 CTTGATACAGCTGTATTAAGACTCTCGACTTTGGAAAGTGCAGAGAGCTGGTCCGAGGA 769  
Qy 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuLlePheGly 240  
Db 770 GAGCCCAATGTTTCATATATATCTCTCTCGTACTACAGGCGCACAGAGCTGATCTTTGGA 829  
Qy 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260  
Db 830 GCCACCGATTACACGCTCTAGTATAGATGTATGTCTCTGAGGCTGTGTGTGGCTGAATTG 889  
Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluLle 280  
Db 890 TTGCTAGGACAACCAATATTTCTGGGGACAGTGGTGTGGATCAGTTGGTGGAAATATA 949  
Qy 281 LysValLeuGlyThrProThrArgGluGlnLleArgGluMetAsnProAsnTyrThrGlu 300  
Db 950 AAGTCTCTAGGAACACCAACAGGAGCAAAATTAGAGAAATGAACCAAAATATACAGAA 1009  
Qy 301 PheLysPheProGlnLleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320  
Db 1010 TTCAAATTCGCCCAATCAAGGCACATCTCTGGACGAAGGCTCTTGGCCGCCCAACTCCA 1069  
Qy 321 ProGluAlaLleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340  
Db 1070 CCAGAGGCAATCGACCTGTGTAGCCGCTCTCTCGAGTACACGCCGACCCGCCGCTAAACA 1129  
Qy 341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360  
Db 1130 CCACTGGAGCTTGTGCACATTCATTTTGTGATGAATTACGGGACCCCAAAATGTCAAACTA 1189  
Qy 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380  
Db 1190 CCAATGGGCGAGACACACCTGCTCTTCACTTTTACCCTCAAGAACTGTCAAGTAAC 1249





Db 1 ATGTGAGGCGGCCAGAACCCCTCTTTGGGAGAGCTGCAAGCGGTGCAGCAGCCT 60  
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACGCGCAGCAAGGTGACACAGTG 120  
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70  
Db 121 GTGGCACTCTCTGGCAGGCTGAGCAGGCGCCCAAGAGCTCAGCTATACAGACACTAAA 180  
QY 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
Db 181 GTGATTGGAAATGGATCATTTGGTGGTATATCAAGCCAACTTTGTGATTGAGAGAA 240  
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 241 CTGGTCGCCATCAAGAAGTATTTCAGGACACAGAGATTTAAGAATCGAGAGCTCCAGATC 300  
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 301 ATGAGAARGCTAGATCACTGTAACATAGTCCGATTGCGTTATTCTTCTACTCCAGTGT 360  
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 361 GAGAGAARGATGAGGTCTATCTTAACTCTGGTCTGACTATGTTCCGAAACAGTATAC 420  
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 421 AGAGTTGCCAGACACTATAGTCAGGCCAACACAGCGCTCCCTGTGATTATGTCAAGTTG 480  
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
Db 481 TATATGTATCAGCTGTTCGAACTTTAGCCCTATATCCATTCCTTTTGGAAATCTGCCATCG 540  
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
Db 541 GATATTAAACCGCAGAACCTCTTTGGTGGATCCTGTACTGCTGTATTAAACCTCTGTGAC 600  
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
Db 601 TTGGGAAGTGCAGAGCAGCTGTCGAGGAGAACCCCAATGTTTCGTATATCTCTCTCGG 660  
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
Db 661 TACTATAGGCGCACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 720  
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
Db 721 TGTCTCTGCTGGCTGTGTGTGGCTGAGCTGTTACTAGGCAACCAATATTTCCAGGGGAT 780  
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
Db 781 AGTGGTGTGGATCAGTTGGTAGAATATCAAGGCTCTGGGAATCCACAGAGGAGCAA 840  
QY 291 IleArgGluMetAsnProHentTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
Db 841 ATCAGAGAATGAACCCAACTACACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 900  
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330  
Db 901 TGGACTTAAGGTCTCTCCGACCCCACTCCCACTCCAGGAGCAATTCGACTGTGTAGCCGCTG 960  
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
Db 961 CTGGAGTATACCAACTGCCCCGACTAACACCACTGGAGCTTGTGCACATTCATTTTTT 1020  
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370  
Db 1021 GATGAATTACGGGACCCAAATGTCAAACCTACCAAAATGGGCGAGACACACCTGCACTCTTC 1080  
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390

Db 1081 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGCTGCTACCATCTTATTCTCCT 1140  
QY 391 HisAlaArgIle 394  
Db 1141 CATGCTCGGATT 1152  
RESULT 10  
US-10-482-524-3  
; Sequence 3, Application US/10482524  
; Publication No. US20040261137A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham PLC  
; APPLICANT: Holder, Julie C  
; TITLE OF INVENTION: Models for Metabolic Disorders  
; FILE REFERENCE: PG4458  
; CURRENT APPLICATION NUMBER: US/10/482,524  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB 0115570.4  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: GB 0205604.2  
; PRIOR FILING DATE: 2002-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-482-524-3  
Alignment Scores:  
Pred. No.: 2,73e-239 Length: 1389  
Score: 2013.00 Matches: 383  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 96.7% Indels: 0  
DB: 9 Gaps: 0  
US-10-733-816-2 (1-394) x US-10-482-524-3 (1-1389)  
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
Db 40 ATGTCAAGGCGGCCAGAACCCCTCTTTGGGAGAGCTGCAAGCGGTGCAGCAGCCT 99  
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACGCGCAGCAAGGTGACACAGTG 159  
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70  
Db 160 GTGGCAACTCTCTGGGCGAGGCTCCAGACAGGCCCAAGAGTTCAGCTATACAGACACTAAA 219  
QY 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
Db 220 GTGATTGGAAATGGATCATTTGGTGGTATATCAAGCCAACTTTGTGATTGAGAGAA 279  
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
Db 280 CTGGTCGCCATCAAGAAGTATTTCAGGACACAGAGATTTAAGAATCGAGAGCTCCAGATC 339  
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTTATTCTTCTACTCCAGTGT 399  
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
Db 400 GAGAGAARGATGAGGTCTATCTTAACTCTGGTCTGAGCTATGTTCCGAAACAGTATAC 459  
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
Db 460 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519  
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190









QY 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis 360  
 DB 1105 CCACTGGAACCTTGCGACATTTCAATTTTGTGAAATACGGACCCCAATATGCAAACTA 1164  
 QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380  
 DB 1165 CCAATGGGGGAGACACACCTGCGCTCTTCAACTTTTACCACCTCAAGAAGTGTCAAGTAAC 1224  
 QY 381 ProProLeuAlaThrLeuLeuLeuProProHisAlaArgile 394  
 DB 1225 CCACCCCTGGCCACCATCTTATCCCTCTCCAGCTCGGATT 1266  
 RESULT 13  
 US-10-613-728-7  
 ; Sequence 7, Application US/10613728  
 ; Publication No. US20040010813A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cincinnati Children's Hospital Medical Center  
 ; APPLICANT: Robbins, Jeffrey  
 ; TITLE OF INVENTION: A ROBUST, INDUCIBLE CARDIAC PREFERRED  
 ; FILE REFERENCE: EXPRESSION SYSTEM FOR TRANSGENESIS  
 ; CURRENT APPLICATION NUMBER: US/10/613,728  
 ; PRIOR FILING DATE: 2003-07-03  
 ; PRIOR FILING DATE: 2003-07-03  
 ; PRIOR FILING DATE: 2002-07-03  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1503  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; LOCATION: (33)...(1295)  
 ; OTHER INFORMATION: GSK-CA  
 US-10-613-728-7  
 Alignment Scores:  
 Pred. No.: 7,34e-239 Length: 1503  
 Score: 2010.00 Matches: 382  
 Percent Similarity: 99.7% Conservative: 1  
 Best Local Similarity: 99.5% Mismatches: 1  
 Query Match: 96.6% Indels: 0  
 DB: 7 Gaps: 0  
 US-10-733-816-2 (1-394) x US-10-613-728-7 (1-1503)  
 QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 DB 33 ATGTGGGGGCGACCGAGAACACCGCGTTTTCGGAGAGCTGCAAGCCAGTGCAGCAGCCT 92  
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
 DB 93 TCAGCTTTTGTAGCATGAAGTTAGCAGAGATAAAGATGCGCAGCAAGGTAAACACAGTA 152  
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70  
 DB 153 GTGGCAACTCTCGGCCAGGCTCTGACAGCCACAGGAAGTCAAGTTATACAGACACGAAA 212  
 QY 71 ValileGlyAsnGlySerPheGlyValValThrGlnAlaLysLeuLysCysAspSerGlyGlu 90  
 DB 213 GTGATTGGAAATGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCTGGAGAA 272  
 QY 91 LeuValAlaLeuLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 DB 273 CTGTTGGCCATCAAGAAGTTCTACAGCAACAGCATTTAAGAACCAGAGAGTCCAGATC 332  
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgThrPheThrSerSerGly 130  
 DB 333 ATGAGAAAGCTAGACCACTGAACATAGTCGAGCTCGGATTCTTCTACTCGAGTGGT 392  
 QY 131 GluLysLysAspGluValThrLeuAsnLeuValLeuAspThrValProGluThrValThr 150

DB 393 GAGAAGAAAGATGAGTCTACCTTAACCTGGTGTGAGATGATGTTCCGGAGACAGGTGAC 452  
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
 DB 453 AGAGTCGCCACAGACATATAGTCGAGCAAGCAGACATCCCTGTGATCTATGTCAAGTTG 512  
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 DB 513 TATATGTATCAGCTGTTCAGAGTCTAGCCCTATATCCATCTTTGGAAATCTGCCATCGA 572  
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 DB 573 GACATTAACCCACAGAACCTCTTGTGGATCCTGTATACAGCTGTATTAATAACTCTGTGAC 632  
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 DB 633 TTTTGAAGTGTCAAAAGCAGCTGTCCGAGGAGAGCCCAATGTTTCATATATCTGTCTCGG 692  
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 DB 693 TACTACAGGCACACAGAGTTGATCTTTGGAGCCACTGATTACAGCTCCAGTATAGATGTA 752  
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
 DB 753 TGGTCTGCAGGCTGTGTGTGGCTGAATTGTTCTAGGACCAACCAATATTTCTGGGAC 812  
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
 DB 813 AGTGGTGTGATCAGTTGGTGGAAATAATAAAGGTCTTAGGAACACCAACAGGGAGCAA 872  
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310  
 DB 873 ATTAGAGAAATGAACCCCAATATATACAGAAATCCCTCAAATCAAGGACATCTCT 932  
 QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuLysSerArgLeu 330  
 DB 933 TGGACAAAGGTCTTCCGGCCCCGAACTCCACACAGAGCAATTGCACCTGTGCAGCCGTCTG 992  
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350  
 DB 993 CTGGAGTACACACCTACCGCCCGGCTAAACACCACTGGAAGCTTTGTGCACATTCATTTTC 1052  
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370  
 DB 1053 GATGAATTTGGGACCCCAATGTCAAACTACCAAAATGGGCGAGACACACCTGCCTCTTC 1112  
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProLeuAlaThrIleLeuIleProPro 390  
 DB 1113 AACTTTTACCACCTCAAGAACTGTCAAGTAACCCCTCTGGCCACCATCTTATCCCTCCA 1172  
 QY 391 HisAlaArgile 394  
 DB 1173 CATGCTCGGATT 1184  
 RESULT 14  
 US-09-866-712-1  
 ; Sequence 1, Application US/09866712  
 ; Patent No. US20020058637A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akihiko TAKASHIMA et al.  
 ; TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY  
 ; INHIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S DISEASE  
 ; KINASE I (AS AMENDED)  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: WENDEROTH, LIND & PONACK  
 ; STREET: 2033 K Street, N.W., #800  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20006  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/866,712  
 FILING DATE: 30-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/216,958  
 FILING DATE: December 21, 1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee Cheng  
 REGISTRATION NUMBER: 40,949  
 REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 721-8200  
 TELEFAX: (202) 721-8250  
 TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 2088 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 ORIGINAL SOURCE:  
 ORGANISM: human being  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-866-712-1

## Alignment Scores:

Pred. No.: 1.25e-238 Length: 2088  
 Score: 2010.00 Matches: 382  
 Percent Similarity: 99.7% Conservative: 1  
 Best Local Similarity: 99.5% Mismatches: 1  
 Query Match: 96.6% Indels: 0  
 DB: 3 Gaps: 0

US-10-733-816-2 (1-394) x US-09-866-712-1 (1-2088)

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 DB 676 TCAGCTTTTGGCAGCATGAAGTTAGCAGAGACAGGACGCGCAGCAAGTGACACAGTG 735  
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrAspThrLys 70  
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 DB 796 CTAATGGAAATGGATCATTTGGTGGTATATCAAGCCAACTTTGTGATTCAGAGAA 855  
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 DB 856 CTGGTCCCATCAAGAAGATTTCAGGACACAGAGATTGAAGATCGAGAGCTCCAGATC 915  
 QY 111 MetArgLysLeuAspHisCysAniIleValArgLeuArgThrPhePheThrSerSerGly 130  
 DB 916 ATCAGAAAGCTAGATCACTCACTAATAGTCCGATGGTGGTATTCTTCTACTCCAGTGT 975  
 QY 131 GluLysLysAspGluValThrLysAsnLeuValLeuAspThrValProGluThrValThr 150  
 DB 976 GAGAAGAAAGATGAGTCTATCTTAATCTGGTCTCGACTATGTTCCGGAACAGTATAC 1035  
 QY 151 AtqValAlaArgHisThrSerArgAlaLysGlnThrLeuProValIleThrValLysLeu 170  
 DB 1036 AGAGTTGCCAGACACTATAGTCAGCCAAACAGACGCTCCCTGTGATTATGTCAGATTG 1095

QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 DB 1096 TATATGATATCAGCTGTTCCGAGTTAGGCTATATCCATTCCTTTGGAATCTCCATCGG 1155  
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 DB 1156 GATATTAAACCGCAGAACCTCTTGTGGATCCTGTATCTGTATTAANAACCTGTGAC 1215  
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerThrIleCysSerArg 230  
 DB 1216 TTTGGAAGTGCAGAGCAGCTGTCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 1275  
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 DB 1276 TACTATAGGCACAGAGTTGATCTTTGGAGCCACTGATATACCTCTAGTATAGATGTA 1335  
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
 DB 1336 TGGTCTGTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 1395  
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290  
 DB 1396 AGTGTGTGGATCAGTTGGTAGAATAATCAAGGTCTCTGGAACTCCCAACAGGAGCAA 1455  
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 ; Sequence 13, Application US/10278759  
 ; Publication No. US20030114382A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walsh, Kenneth  
 ; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells  
 ; FILE REFERENCE: S01237.70030.US  
 ; CURRENT APPLICATION NUMBER: US/10/278,759  
 ; CURRENT FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/350160  
 ; PRIOR FILING DATE: 2001-10-29  
 ; PRIOR APPLICATION NUMBER: US 60/337905  
 ; PRIOR FILING DATE: 2001-11-13  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
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 ; LENGTH: 1639  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-278-759-13

Alignment Scores: 4.06e-237 Length: 1639  
 Pred. No.: 1996.50 Matches: 383  
 Score:

Percent Similarity: 96.5% Conservative: 0  
Best Local Similarity: 96.5% Mismatches: 1  
Query Match: 95.9% Indels: 13  
DB: 6 Gaps: 1

US-10-733-816-2 (1-394) x US-10-278-759-13 (1-1639)

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DB	293	TCAGCTTTTGGCAGCATGAAGTTAGCAGAGACAGGACGCGCAGGAGGTGACAAACGTG	352
QY	51	ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys	70
DB	353	GTGGCAACTCTCGGCAGGGTCCAGACAGGCCACAGAAAGTCAGCTATACAGACACTAAA	412
QY	71	ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu	90
DB	413	GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGGAA	472
QY	91	LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle	110
DB	473	CTGGTCGCCATCAAGAAAGTATTTCAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC	532
QY	111	MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSergly	130
DB	533	ATCAGAAAGCTAGATCACTTAACATAGTCCGATTGGTTATTTCTTCTACTCCAGTGT	592
QY	131	GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr	150
DB	593	GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGTGACTATGTTCGGAAACAGTATAC	652
QY	151	ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu	170
DB	653	AGAGTTGCCAGACACTATATGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAGATTG	712
QY	171	TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg	190
DB	713	TATATGTATCAGCTGTTCCGAAGTTTAGCTATATCCATTCCTTGGAACTCGCCATCGG	772
QY	191	AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp	210
DB	773	GATATTAAACCGCAGAACCTCTTGTGGATCCTGATCTGTATTTAAAACTCTGTGAC	832
QY	211	PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg	230
DB	833	TTTGGAAAGTCAAGACAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCGG	892
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DB	893	TACTATAGGCCACCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA	952
QY	251	TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAsp	270
DB	953	TGGTCTGCTGGCTGTGTGGTGGCTGAGCTGTTACTAGGCAACCAATATTTCCAGGGGAT	1012
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DB	1073	ATCAGAGAAATGAACCAAACTACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT	1132
QY	311	TrpThrLys-----ValPheArgPro	317
DB	1133	TGGACTAAGGATTCGTCCAGAACACAGGACATTTACCTCCAGAGTGGCGGTCTTCCGACCC	1192
QY	318	ArgThrProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAla	337

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Job time : 1496 secs

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1253 CGACTAACACCACTGGAAGCTTGTGCACATTCATTTTGTGATTAATTCGGGACCCAAAT 1312  
358 ValLysHisProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeu 377  
1313 GTCAAACTACCAAAATGGGAGAGACACCTGCACTCTTCAACTTCACCACTCAAGAACTG 1372  
378 SerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArgIle 394  
1373 TCAAGTAAATCCACCTCTGGCTACCACTCTTATCTCTCTCATGCTCGGATT 1423

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2006, 01:40:30 ; Search time 248 Seconds  
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Total number of hits satisfying chosen parameters: 4660992

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1996.5	95.9	1302	8	US-11-299-324-3
3	1996.5	95.9	1639	8	US-11-283-329-215
4	1974	94.9	1319	8	US-11-299-324-2
5	1961.5	94.3	1388	8	US-11-299-324-1
6	1919	92.2	1164	8	US-11-299-324-6
7	1808	86.9	1167	8	US-11-299-324-4

Sequence 9, Appli  
Sequence 3, Appli  
Sequence 215, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 6, Appli

Sequence 347876,  
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Sequence 431255,  
Sequence 28735, A  
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Sequence 13, Appli  
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ALIGNMENTS

RESULT 1  
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; Sequence 9, Application US/11299324  
; Publication No. US20060127388A1  
; GENERAL INFORMATION:  
; APPLICANT: Cain, Michael  
; APPLICANT: Jaworsky, Paul J  
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof  
; FILE REFERENCE: WYE-052  
; CURRENT APPLICATION NUMBER: US/11/299,324  
; CURRENT FILING DATE: 2005-12-09  
; PRIOR APPLICATION NUMBER: US 60/634,813  
; PRIOR FILING DATE: 2004-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 9  
; LENGTH: 1263  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-299-324-9

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Pred. No.: 2 49e-215 Length: 1263  
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Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 96.7% Indels: 0  
DB: 8 Gaps: 0

US-10-733-816-2 (1-394) x US-11-299-324-9 (1-1263)

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QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrThrVal 50
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Db 361 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGTGGAGTATGTTCCGGAAACAGTATAC 420
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; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCES: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; PRIOR FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-3
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Pred. No.: 1,84e-213 Length: 1302
Score: 1996.50 Matches: 383
Percent Similarity: 96.5% Conservative: 0
Best Local Similarity: 96.5% Mismatches: 1
Query Match: 95.9% Indels: 13
DB: Gaps: 1
US-10-733-816-2 (1-394) x US-11-299-324-3 (1-1302)
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Db 1 ATGTCAGGGCGGCCAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGGTGCAGACGCT 60
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QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 361 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGTGGAGTATGTTCCGGAAACAGTATAC 420
QY 151 ArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 421 AGAGTTGCCAGACACTATAGTCAGGCCAAACACAGACGCTCCCTGTGATTATGTCAAGTTG 480
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 481 TATATGTATCAGCTGTTCCGAAGTTAGCCATATATCCATTCTCTTGGAAATCTGCCATCGG 540
```







Db 1193 CGAATCCACCGAGGCAATTGCTGTGTAGCGCTCTGCTGAGGTATACACCACTGCC 1252  
 Qy 338 ArgLeuThrProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsn 357  
 Db 1253 CGACTAACACCACTGGAAGCTTGTGCACATTCATTTTTCATGAATTCAGGACCCAAAT 1312  
 Qy 358 ValIleHisProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeu 377  
 Db 1313 GTCAAACTACCAATGGCGAGACACACCTGCACTCTTCAACTTCACCACTCAAGAACTG 1372  
 Qy 378 SerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArgile 394  
 Db 1373 TCAAGTAATCCACTCTGCTGCTACCATCTTATTCCTCTCATGCTCGGATT 1423

## RESULT 4

US-11-299-324-2  
 ; Sequence 2, Application US/11299324  
 ; Publication No. US20060127388A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cain, Michael  
 ; APPLICANT: Yaworsky, Paul J  
 ; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof  
 ; FILE REFERENCE: WYE-052  
 ; CURRENT APPLICATION NUMBER: US/11/299,324  
 ; CURRENT FILING DATE: 2005-12-09  
 ; PRIOR APPLICATION NUMBER: US 60/634,813  
 ; PRIOR FILING DATE: 2004-12-10  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 2  
 ; LENGTH: 1319  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-11-299-324-2

Alignment Scores:  
 Pred. No.: 6,23e-211 Length: 1319  
 Score: 1974.00 Matches: 382  
 Percent Similarity: 94.8% Conservative: 0  
 Best Local Similarity: 94.8% Mismatches: 2  
 Query Match: 94.9% Indels: 20  
 DB: 8 Gaps: 1

US-10-733-816-2 (1-394) x US-11-299-324-2 (1-1319)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
 Db 1 ATGTCAGGGCGGCCAGAACCACTCTCTTTGGAGAGCTGCAAGCGGTGCAGCAGCCT 60  
 Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50  
 Db 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAAGACGCGCAGCAAGGTGCAACAGTG 120  
 Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70  
 Db 121 GTGGCAACTCTGGCGAGGTCCAGACAGGCCACCAAGAACTGAGTATACAGACACTAAA 180  
 Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90  
 Db 181 GTGATGGAAATGGATCATTTGGTGGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 240  
 Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110  
 Db 241 CTGGTCGCCATCAAGAAGATTATTCAGGACAAGAGATTTAAGAAATCAGAGCTCCAGATC 300  
 Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130  
 Db 301 ATGAGAAGCTAGATCATCTGAACATAGTCCGATGGGTATTCTTCTACTCCAGTGGT 360  
 Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150  
 Db 361 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTGTGGACTATGTTCCGGAAACAGTATAC 420

Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170  
 Db 421 AGAGTTTGCAGACACTATAGTCAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480  
 Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190  
 Db 481 TATATGTATCAGCTGTTCGAAGTTTAGCTATATCCATTCCTTTTGAATTCGCCATCG 540  
 Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210  
 Db 541 GATATTAAACCCGAGAACCTCTTTTGGATCTCTGATCTGCTGATTAATAAACTCTGTGAC 600  
 Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230  
 Db 601 TTTGGAAGTGCRAAGCAGCTGTGTCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCG 660  
 Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250  
 Db 661 TACTATAGGCGCACAGAGTTGATCTTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 720  
 Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270  
 Db 721 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTTACTAGGACAACCAATATTTCCAGGGGAT 780  
 Qy 271 SerGlyValAspGlnLeuValGluIleIleLysVal----- 282  
 Db 781 AGTGGTGTGGATCAGTTGGTAGAAATTAATCAAGGT-GTCCCCCAGAAATTCATATAAGC 839  
 Qy 283 -----LeuGlyThrProThrArgGluGlnIle 291  
 Db 840 AATCTAGGAAGTTTTCGACCTCGGAAAGCTGCTCTCGGAACCTCCAACAGGAGCAATC 899  
 Qy 292 ArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyr 311  
 Db 900 AGAGAAATGAACCCCAAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCTTG 959  
 Qy 312 ThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgGluLeu 331  
 Db 960 ACTAAGGTCTTTCGACCCCGAACTCCACCGAGGCAATGCACTGTGTAGCCGTCTGCTG 1019  
 Qy 332 GluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPheAsp 351  
 Db 1020 GAGTATACACCAACTGCGCGACTTAACACCACTGGAAGCTGTGCACATTCATTTTGTAT 1079  
 Qy 352 GluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsn 371  
 Db 1080 GAATTCAGGAGCCCAAAATGTCAAACTTACCAAAATGGCGGAGACACACCTGCACCTTCAAC 1139  
 Qy 372 PheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProProHis 391  
 Db 1140 TTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCCTCAT 1199  
 Qy 392 AlaArgile 394  
 Db 1200 GCTCGGATT 1208

## RESULT 5

US-11-299-324-1  
 ; Sequence 1, Application US/11299324  
 ; Publication No. US20060127388A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cain, Michael  
 ; APPLICANT: Yaworsky, Paul J  
 ; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof  
 ; FILE REFERENCE: WYE-052  
 ; CURRENT APPLICATION NUMBER: US/11/299,324  
 ; CURRENT FILING DATE: 2005-12-09  
 ; PRIOR APPLICATION NUMBER: US 60/634,813  
 ; PRIOR FILING DATE: 2004-12-10  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1  
 ; LENGTH: 1388

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-299-324-1
Alignment Scores:
Pred. No.: 1-69e-209 Length: 1388
Score: 1961.50 Matches: 382
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 2
Query Match: 94.3% Indels: 43
DB: 8 Gaps: 1
US-10-733-816-2 (1-394) x US-11-299-324-1 (1-1388)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 1 ATGTCAAGGCGCGCCAGAACCACTCTCTTTGCGAGAGCTGCAAGCGGTGCAGCAGCT 60
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
DB 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGACCGCAGCAAGGTGACAAAGTG 120
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
DB 121 GTGGCAACTCTCTGGCAGGCTCAGACAGGCCACACAGAGTCACTTATACAGACATCAA 180
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
DB 181 GTGATTGGAAATGGATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGAGAA 240
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 241 CTGGTCGCCATCAAGAAAGATTATTCAGGACACAGAGATTTAAGAAATCGAGACTCCAGATC 300
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPheTyrSerSerGly 130
DB 301 ATGAGAAAGTAGATCACTGTAACTAGTCCGATTCGGATTATTCCTCTACTCCAGTGGT 360
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 361 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATCTTCGGAAACAGTATAC 420
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
DB 421 AGAGTTGCCACAGACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 480
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 481 TATATGTATCAGCTGTTCGAGTGTAGCCCTATATCCATTCCTTTGGAATCTGCCATCGG 540
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 541 GATATTAAACCGCAGAACCTCTTGTGGATCCCTGATCTGCTGATTATAAACTCTGTGAC 600
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
DB 601 TTTTGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAAATGTTTCGTATATCTCTTCTCGG 660
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyValAlaThrAspTyrThrSerSerIle----- 248
DB 661 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTAT-AGGTCA 719
QY 248 ----- 248
DB 720 ATAAAAAGTAGTCACTGGACCAAGATTTCAGTCTCTCTTGATAGTACATCTCACCACA 779
QY 248 ----- 248
DB 780 TCAGACCTTTAAAAATTTTGTGTCAACCATTTACTGTTCCTTCTTCTCTCTCCGTACT 839
QY 249 AspValTyrSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePhePro 268
DB 840 GATGTATGTCTGCTGGCTGTGTGTGGCTGAGCTGTGTACTAGGACAAACCAATATTTCGA 899
QY 269 GlyAspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArg 288
DB 900 GGGGATAGTGTGTGGATCAGTTGGTAGAAATAATCAAGTCTCTGGAACTCCCAACAGG 959
QY 289 GluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAla 308
DB 960 GAGCAATCAGAGAAATGAACCAACTACACAGAATTTAAATTCCTCTCAAAATTAAGGCA 1019
QY 309 HisProTyrThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSer 328
DB 1020 CATCTTTGGACTAAGTCTTCCGACCCCGAACTCCACCGGAGGCAATTCGACTGTGTAGC 1079
QY 329 ArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSer 348
DB 1080 CGTCTCTGGAGTATACACCACTGCCCGACTAACCACTTGGAAAGTTGTGCACATTC 1139
QY 349 PhePheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAla 368
DB 1140 TTTTGTGATGAATTCAGGACCCCAATGTCAAACTACCAATGGCGAGACACACCTGCA 1199
QY 369 LeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIle 388
DB 1200 CTCTTCACTTCACTCAAGAACTGTCAAGTAATCCACTCTGTGCTACCATCTTATT 1259
QY 389 ProProHisAlaArgIle 394
DB 1260 CCTCCTCATGCTCGGATT 1277
RESULT 6
US-11-299-324-6
; Sequence 6, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-6
Alignment Scores:
Pred. No.: 7-51e-205 Length: 1164
Score: 1919.00 Matches: 364
Percent Similarity: 99.5% Conservative: 3
Best Local Similarity: 98.6% Mismatches: 2
Query Match: 92.2% Indels: 0
DB: 8 Gaps: 0
US-10-733-816-2 (1-394) x US-11-299-324-6 (1-1164)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 1 ATGTCAAGGCGCGCCAGAACCACTCTCTTTGCGAGAGCTGCAAGCGGTGCAGCAGCT 60
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
DB 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGACCGCAGCAAGGTGACAAAGTG 120
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
DB 121 GTGGCAACTCTCTGGCAGGCTCAGACAGGCCACACAGAGTCACTTATACAGACATCAA 180
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
```

181	Db	GTGATTGGAAATGGATCATTTGGTGTGGTATATCAAGCCAAACTTTTGTGATTCAGAGAA	240
91	Qy	LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle	110
241	Db	CTGGTCCCATCAAGAAAGATTTCGAGGACACAGAGATTTAAGAATCGAGAGCTCCAGATC	300
111	Qy	MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly	130
301	Db	ATGAGAAGCTAGATCATCTGTAACATAGTCGGAATGGGTATTCTTCTACTCCAGTGGT	360
131	Qy	GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr	150
361	Db	GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGAAAACAGTATAC	420
151	Qy	ArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu	170
421	Db	AGAGTTGCCACAGACACTATAGTCGAGGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG	480
171	Qy	TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg	190
481	Db	TATATGTATCAGCTGTTCCGAAGTTTAGCTATATCAATTCCTTTGGAATCTGCCATCGG	540
191	Qy	AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp	210
541	Db	GATATTAAACCGCAGAACCTCTTGTTGGATCCTGATACCTGCTGTATTAAACTCTGTGAC	600
211	Qy	PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg	230
601	Db	TTTGGAAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCGG	660
231	Qy	TyrTyrArgAlaProGluLeuLysPheGlyValaThrAspTyrThrSerSerIleAspVal	250
661	Db	TACTATAGGGCACAGAGTTGATCTTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA	720
251	Qy	TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp	270
721	Db	TGGTCTGCTGGCTGTGTGTTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGAT	780
271	Qy	SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln	290
781	Db	AGTGGTGTGATCAGTTGGTAGAAATATCAAGGTCTTGGGAATCTCCAAACAGGAGGACAA	840
291	Qy	IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro	310
841	Db	ATCAGAGAAATGAACCCAACTACACAGAAATTAAATTCCTCAAATTAAGGCACATCCT	900
311	Qy	TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu	330
901	Db	TGGACTAAGGTCTTCCGACCCGAACTCCACCGAGGCAATTCACCTGTGTAGCCGCTG	960
331	Qy	LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe	350
961	Db	CTGAGATATACCAACTGCCCGGACTAACACCACTGGAAGCTGTGTGCACATTTCAATTTT	1020
351	Qy	AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe	370
1021	Db	GATGAATTACGGGACCCAAATGTCAAACTACCAATGGCGAGACACACCTGCATCTTTC	1080
371	Qy	AsnPheThrThrGlnGluLeuSerSer	379
1081	Db	AACTTCACCACTCAAGATGCTAAATACT	1107





326	Db	GGCGAGGAGGACGAGGAGGCGCGCGCAGACGACTAGTCTCCCGCGCGCC-----	376
27	Qy	ValGlnGlnProSerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLys	46
377	Db	-----GGGTGAAGCTGGCGCGT-----GACAGCGGGAAG	406
47	Qy	ValThrThrValValAlaIaThrProGlyGlnGlyProAspArgProGlnGlnValSerTyr	66
407	Db	GTGACCAACAGTCGTAGCGACACTCTTAGGCCCAAGGCCAGAGCGCTCCCAAGAAGTGGCTTAC	466
67	Qy	ThrAspThrLysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCys	86
467	Db	ACGACATCAAAAGTATGGCAATGGCTCATTTGGGTCTGTACACAGGACAGGCTGGCA	526
87	Qy	AspSerGlyGluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArg	106
527	Db	GAGACCAGGGAACTAGTCGCCATCAAGAAGGTTCTCCAGGACAAAGAGGTTCAAGAACCGA	586
107	Qy	GluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePhe	126
587	Db	GAGCTGCAGATCATGCGTAGCTGCAGCACCTGCAATATTGTGAGGCTGAGATACTTTTTC	646
127	Qy	TyrSerSerGlyGluLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPro	146
647	Db	TACTCCAGTGGCAGAGAAGAAGAGAGCTTTACTTAATCTGGTGCTGGAAATATGTGCC	706
147	Qy	GluThrValTyrArgValAlaAraHisTyrSerArgAlaLysGlnThrLeuProValIle	166
707	Db	GAGACAGTGTACCGGTTGGCCGCCACTTCACCAAGGCCAAGTTGACCATCCCTATCCTC	766
167	Qy	TyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGly	186
767	Db	TATGTCAAGGTGTACATGTATACAGCTCTTCGCGAGCTTGGCTACATCCACTCCAGGGC	826
187	Qy	IleCysHisArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeu	206
827	Db	GTGTGTCAACGCGACATCAAGCCCAAGAACTGCTGTGTGACCTGACACTGTCTGTCTC	886
207	Qy	LysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyr	226
887	Db	AAGCTCTCGATTTTGGCAGTGCAAAGCAGTTGTGTCCGAGGGAGCCCAATGCTCTCTAC	946
227	Qy	IleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSer	246
947	Db	ATCTGTCTCGCTACTACCGGGCCCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCA	1006
247	Qy	SerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIle	266
1007	Db	TCCATCATGTTTGGTCAGCTGGCTGTGTACTGTCGACAGCTCTCTTTGGGCGACCCATC	1066
267	Qy	PheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrPro	286
1067	Db	TTCCCTGGGACAGTGGGTGGACAGCTGTGTGAGATCATCAAGGTGCTGGGAACACCA	1126
287	Qy	ThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIle	306
1127	Db	ACCGGGACAAATCCGAGAGATGAACCCCAACTACACGAGTTCAAGTTCCCTCAGATT	1186
307	Qy	LysAlaHisProThrTrpLysValPheArgProArgThrProProGluAlaIleAlaLeu	326
1187	Db	AAAGCTCACCCCTGCACAAAGGTGTTCAAATCTCGAAACGCCGCGCAGAGGCCATCGCGCTC	1246
327	Qy	CysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAla	346
1247	Db	TGCTCTAGCTGTCTGGAGTACACCCCATCTCAAGGCTCTCCCCACATAGAGGCTGTGCG	1306
347	Qy	HisSerPhePheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThr	366
1307	Db	CACAGCTCTTTGATGAACTGCGATGTCTGGAAACCCAGCTGCCTTACACCGGCCACTT	1366
367	Qy	ProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIle	386
1367	Db	CCCCCTCTTCAACTTCAGTGTGGTGAACCTCTCCATCCAAACCGTCTCTCAACGCCATT	1426







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Db      1118 CAAATCCGAGAGATGAACCCCAACTACCGAGTTCAAGTTCCCTCAGATTAAGCTCAC 1177
Qy      310 ProTfPThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArg 329
Db      1178 CCCTGGACAAGAGTGTTCAAATCTCGAACCAGCCGAGAGCCATCGCGCTCTGCTCTAGC 1237
Qy      330 LeuLeuGluTyThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
Db      1238 CTGCTGGAGTACACCCCATCCTCAAGGCTCTCCCACTAGAGGCGCTGTGGCACAGCTTC 1297
Qy      350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369
Db      1298 TTTGATGAACCTGGATGCTGTGGGAACCCAGCTGCTTAACAAACCGCCCACTTCCCCCTTC 1357
Qy      370 PheAsnPheThrThrGlnGluLeuLeuSerSerAsnProProLeuAlaThrIleLeuIleR 389
Db      1358 TTCACCTTCACTGCTGTGTGAACCTTCATCCACACCGTCTCTCAACGCCATTTCTCATCC 1417
Qy      390 ProHisAlaArg 393
Db      1418 CCTCACTTGAGG 1429

RESULT 12
US-10-553-520-84
; Sequence 84, Application US/10553520
; Publication No. US2006018885A1
; GENERAL INFORMATION:
; APPLICANT: Bodian, Dale
; APPLICANT: Daouti, Sherif
; APPLICANT: Kumar, Chandrika
; APPLICANT: Latario, Brian
; APPLICANT: Quintavalla, Joseph
; TITLE OF INVENTION: High throughput functional genomic
; TITLE OF INVENTION: screening methods for osteoarthritis
; FILE REFERENCE: 4-33178
; CURRENT APPLICATION NUMBER: US/10/553,520
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/463,933
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-553-520-84

Alignment Scores:
Pred. No.: 1,05e-169 Length: 2169
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: 6 Gaps: 4

US-10-733-816-2 (1-394) x US-10-553-520-84 (1-2169)
Qy      5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db      130 CCTTCGGGAGGCGGCGCCCTGGGGGCTCGGGGAGGCGGAGCTAGCTAGTTCGCGGAG-- 186
Qy      24 CysLysPro-----ValGlnGln 29
Db      187 -----CCCGGCGGCGGAGGCGGAGGCGGCGGCGGCGGCGGCGGCTCGGCTCCGGC 240
Qy      30 ProSerAlaPheGlySerMetLys----- 37
Db      241 CCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300
Qy      37 ----- 37
Db      301 TCAGAGCTCCGGGGGTGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 360

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QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 361 GGCACCTAGCTCCCGCGCGCGGGTGAAGCTGGCGTGCACAGCGGGAAGGTGACACA 420
QY 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrAspThr 69
Db 421 GTCTAGCCACTTAGGCCAAGGCCCGACAGCGCTCCCAAGAGTGGCTTACACGGACATC 480
QY 70 LysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89
Db 481 AAAGTGATTGGCAATGGCTCATTTGGGGTGGTGTACAGGACCGCTGGCAGAGACCGAG 540
QY 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109
Db 541 GAATAGTCGCCATCAAGAGGTTCTCCAGGACAAGAGGTTCAAGAACCCAGAGCTGCAG 600
QY 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSer 129
Db 601 ATCATGGTAAAGCTGGACCACTGCATATTTGTGAGGCTGAGATACCTTTTCTACTCCAGT 660
QY 130 GlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149
Db 661 GCGAGAGAAGAACGACGAGCTTACCTAAATCTGGTGTGGAATATGTGCCCGAGACAGTG 720
QY 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 721 TACCGGGTGGCCGCCACTTCACCAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAG 780
QY 170 LeuTyrMetTyrGlnLeuPheAsgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189
Db 781 GTGTACATGTACAGCTCTTCCGAGCTTGGCCCTACATCCACTCCAGGGCGGTGTCCAC 840
QY 190 ArgAspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCys 209
Db 841 CGCGACATCAAGCCCAAGACCTGCTGGTGAGCCCTGACACTGCTGTCTCAAGCTCTGC 900
QY 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229
Db 901 GATTTTGGCAGTGCAAAGCAGTGTGTCGAGGGGAGGCCCAATGTCTCTCATCTGTCTCT 960
QY 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyValaThrAspTyrThrSerSerIleAsp 249
Db 961 CGCTACTACCGGGCCCGACAGCTCATCTTTGGAGCCACTGATTACACTCATCATCATGAT 1020
QY 250 ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269
Db 1021 GTTTGGTCACTGGCTGTGTACTGGCAGAGCTCTCTTGGGCCAGCCCATCTTCCCTGGG 1080
QY 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289
Db 1081 GACAGTGGGTGGACCAAGCTGGTGGAGATCATCAAGGTGTGGGAACACCAACCCGGAA 1140
QY 290 GlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHis 309
Db 1141 CAAATCCGAGAGATGAACCCCACTACACGAGTTCAAGTTCCCTCAGATTAAGCTCAC 1200
QY 310 ProTrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArg 329
Db 1201 CCCTGGCAAAAGGTGTTCAAATCTCGAAGCCGCGCAGAGCCATCGCGCTCTGTCTTAGC 1260
QY 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
Db 1261 CTGCTGAGTACACCCCATCTCAAGGCTCTCCCACTAGAGGCTGTGGCAGAGCTTC 1320
QY 350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369
Db 1321 TTTGATGAATGCGATGCTGGGAACCCAGCTGCTTAACACCCGCCACTTCCCTCTC 1380
QY 370 PheAsnPheThrThrGlnGluSerSerAsnProProIleAlaThrIleLeuIlePro 389
Db 1381 TTCAACTTCAGTGTGGTGAACCTCTCCATCCAAACCGCTCTCTCAACGCCACTCTCATCCCT 1440
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QY 390 ProHisAlaArg 393
Db 1441 CCTCACTTGAGG 1452

RESULT 13
US-11-266-748A-56261
; Sequence 56261, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCES: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 56261
; LENGTH: 2200
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-56261

Alignment Scores:
Pred. No.: 1,07e-169 Length: 2200
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: 8 Gaps: 4

US-10-733-816-2 (1-394) x US-11-266-748A-56261 (1-2200)

QY 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db 135 CCTTCGGAGAGCGGCCCTCGGGGCTCGGGCAGCGCGGAGCTAGCTCGTTTCGGGAG--- 191
QY 24 CysLysPro-----ValGlnGln 29
Db 192 -----CCCGCGCGGAGCGGAGGCGGCGGCGGCCCGGAGGCTCGGCTCCGGC 245
QY 30 ProSerAlaPheGlySerMetLys----- 37
Db 246 CCAGCGGCACCGCGCGCGGAAAGCATCTGTCTGGGCCCATGTGTGGGGCGTCTGGGGGCC 305
QY 37 ----- 37
Db 306 TCGAGCTCCGGGGGTGGACCCCGCGCGCAGCGGAGGAGGAGCGGAGGCGCCCGCGGCA 365
QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 366 GGCACCTAGCTTCCCGCGCGCGGGGTGAAGCTGGCCGCTGCACAGCGGGAAGGTGACACA 425
QY 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69
Db 501 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69
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Db 426 GTCTAGCACTCTAGCCCAAGGCCAGAGCGCTCCCAAGAGTGGCTTACACGGACATC 485  
Qy 70 LysValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89  
Db 486 AAAGTGATTGGCAATGGCTCATTTGGGGCTCGTGTACAGGACCGGCTGGCAGACCCAGG 545  
Qy 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109  
Db 546 GAACATAGTCCCATCAAGAGGTTCTCCAGACAAGAGGTTCAAGAACCCGAGAGCTCAG 605  
Qy 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSer 129  
Db 606 ATCATGCGTAAGCTGGACCACTGCAATATTGTGAGGCTGAGATACATTTTCTACTCCAGT 665  
Qy 130 GlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149  
Db 666 GCGCAGAAGAAGACGAGCTTTACCTAAATCTGGTCTGGAATATGTGCCGAGACAGTG 725  
Qy 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169  
Db 726 TACCGGGTGGCCGCCCACTTCAACAAGGCCAAGTTGACCACTCCATCTCTATGTCAAG 785  
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189  
Db 786 GTGTACATGTACCAAGCTCTTCCGAGCTTGGCCCTACATCCACTCCAGGGCGGTGTCTAC 845  
Qy 190 ArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCys 209  
Db 846 CGCGACATCAAGCCCCAGAACCTGCTGGTGGACCTGACACTGTCTCTCAAGCTCTGC 905  
Qy 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229  
Db 906 GATTTTGGCAGTGCAAGACAGTGTGGTCCGAGGGAGGCCAATGTCTCCTACATCTGTCT 965  
Qy 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyValaThrAspTyrThrSerSerIleAsp 249  
Db 966 CGCTACTACCGGGCCCCAGAGCTCACTTTGGAGCCACTGATTACACTCATCTCATCTCAT 1025  
Qy 250 ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269  
Db 1026 GTTTGGTTCAGCTGGCTGTGTACTGGCAGAGCTCCTCTTGGCCAGCCCATCTTCCCTGGG 1085  
Qy 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289  
Db 1086 GACAGTGGGTGGACCAAGCTGGTGGAGATCATCAAGGTGCTGGGAACACCAACCCGGGAA 1145  
Qy 290 GlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHis 309  
Db 1146 CAATCCGAGAGATGAACCCCACTACACGGAGTTCAAGTTCCCTCAGATTAAAGCTCAC 1205  
Qy 310 ProTrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArg 329  
Db 1206 CCCTGGACAAAGTGTTCAAATCTCGAACCGCCAGAGGCCATCGCGCTCTGCTCTAGC 1265  
Qy 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349  
Db 1266 CTGCTGGAGTACACCCCATCTCAAGGCTCTCCCCACTAGAGGCTGTGGCCACAGCTTC 1325  
Qy 350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369  
Db 1326 TTTGATGAATCGGATGCTGGGAACCCAGCTGCTTAACAAACCGCCCACTTCCCCCTCTC 1385  
Qy 370 PheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuPro 389  
Db 1386 TTCAACTTTCAGTGTGGTGAATCTTCCATCCACCGCTCTCTCAAGCCCATCTCATCCCT 1445  
Qy 390 ProHisAlaArg 393  
Db 1446 CCTCACTTGAGG 1457

RESULT 14

US-10-795-135-4

; Sequence, 4, Application US/10795135

; Publication No. US20060099599A1  
; GENERAL INFORMATION:  
; APPLICANT: HEBERLEIN, ULRIKE  
; APPLICANT: WOLFE, FRED  
; TITLE OF INVENTION: THE ROLE OF GLYCOGEN SYNTHASE KINASE-3 AND TETRASPANINS IN  
; TITLE OF INVENTION: ETHANOL-INDUCED BEHAVIORS  
; FILE REFERENCE: 316T-002010US  
; CURRENT APPLICATION NUMBER: US/10/795,135  
; PRIOR FILING DATE: 2004-03-05  
; PRIOR APPLICATION NUMBER: US60/452,486  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 1545  
; TYPE: DNA  
; ORGANISM: Drosophila sp.  
US-10-795-135-4

Alignment Scores: 7.43e-168 Length: 1545  
Pred. No.: 1590.50 Matches: 305  
Score: 88.0% Conservative: 32  
Percent Similarity: 79.6% Mismatches: 41  
Best Local Similarity: 76.4% Indels: 5  
Query Match: 6 Gaps: 4  
DB:

US-10-733-816-2 (1-394) x US-10-795-135-4 (1-1545)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30  
Db 1 ATGAGCGGTGCTCAAGAACTTCTCTCTCCGCGAGGGCAACAAA-----CAGTCGCCG 54  
Qy 31 Ser---AlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThr 49  
Db 55 AGTTTGGTGTGGCGCGCGTCAAAACATGC--AGTCGCATGGTCTTAAATCACAACA 111  
Qy 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69  
Db 112 GTTGTGTCAACACCCGCCAAGGCACCGATCGGTACAGAGGTCTCTATACAGACACA 171  
Qy 70 LysValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89  
Db 172 AAGTTCATCGGCATGGCAGCTTCGGCGTGTCTCAGGCAAGCTCTCGGATACCCGGC 231  
Qy 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109  
Db 232 GAATCGTGGCATCAAAAAGTTTACAGACAGACGATTTAAGATCCGGAATTCGCA 291  
Qy 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSer 129  
Db 292 ATAATCGCAAAATGGAGCATTTGTAATATTGTGAAGCTTTGTACTTTTCTATTCAGT 351  
Qy 130 GlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149  
Db 352 GGTGAAGAGCGTATGAAGTATTTTGAATTTAGTCTCTCGAATATATATACAGAACCGTA 411  
Qy 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169  
Db 412 TACAAAGTGGCTGCCAATATGCAAAACCAACCAACGATACCACTTATTCGG 471  
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189  
Db 472 CTCTACATGTATCACTGTTCAGAGTTTGGCCCTACATCCACTCGCTGGGCAATTTGCCAT 531  
Qy 190 ArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCys 209  
Db 532 CGTGATATCAAGCGCAGAAATCTTCTGCTCGATCCGAGACGGCTGTGTGAAAGCTCTGT 591  
Qy 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229  
Db 592 GACTTTGGCAGCCCAACCAAGCTGTGTCACGGCGCCGAATGTATCTATATCTGCTCC 651

```
QY 230 ArgTyrThrArgAlaProGluLeuLeuPheGlyAlaThrAspTyrThrSerSerIleAsp 249
|||
Db 652 CGGTATTATACCGCCCGAGCTCATCTTTGGCGCCATCAATTATATACAAAGATCGAT 711
|||
QY 250 ValTyrSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269
|||
Db 712 GTCTGGAGTCCCGTGGCTTTGGCGCAACTGCTGCTGGCCAGCCCATCTTCCCTGGC 771
|||
QY 270 AspSerGlyValAspGlnLeuValGluIleLeuValLeuGlyThrProThrArgGlu 289
|||
Db 772 GATTCGGTGTGGATCAGTCCGTCGAGGTATCAAGGTCTGGGCAACACCGACAAGAGAA 831
|||
QY 290 GlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHis 309
|||
Db 832 CAGATACGCGAATGAATCAAACTACACGGAATTCAAGTTCCCTCAGATTAAGAGTCAT 891
|||
QY 310 ProTyrThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArg 329
|||
Db 892 CCATGGCAGAAAGTTTCCGTATACGCACTCCCTACAGAAGCTATCAACTTGGTGCCTG 951
|||
QY 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
|||
Db 952 CTGCTCAGTATACGCCAGTCAGGATCACACGCTCAAGGCTGCGCACATCCGCTTC 1011
|||
QY 350 PheAspGluLeuArg---AspProAsnValLysHisProHengLysArgAspThrProAla 368
|||
Db 1012 TTCATGAGTACGCAATGGAGGGTAAATCACACCTTGCCCAACGCTCGCATATGCCGCCG 1071
|||
QY 369 LeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIle 388
|||
Db 1072 CTGTTCAACTTCACAGAGCATGAGCTCTCAATACAGCCAGCTAGTGCCGCGAGTTGTG 1131
|||
QY 389 ProProHis 391
|||
Db 1132 CCCAAGCAT 1140
|||
RESULT 15
US-11-299-324-13
; Sequence 13, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WFS-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-13
Alignment Scores:
Pred. No.: 1.05e-148 Length: 837
Score: 1416.00 Matches: 272
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 68.0% Indels: 0
DB: 8 Gaps: 0
US-10-733-816-2 (1-394) x US-11-299-324-13 (1-837)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
|||
Db 1 ATGTACAGGGCGGCCAGAACCCACCCTCTCTTTGGAGAGCTGCAAGCGCGTGCAGACCT 60
|||
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
|||
```

```
Db 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACAGCGCAGCAAGGTGACACACAGTG 120
|||
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
|||
Db 121 GTGGCAACTCTCTGGCGAGGTCCAGACAGGCCCAAGAAAGTCAGCTATACAGACACTAAA 180
|||
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuLysCysAspSerGlyGlu 90
|||
Db 181 GTGATTTGGAAATGGATCATTTGGTGGTATATCAAGCCCAACTTTGTGATTCAGAGAA 240
|||
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
|||
Db 241 CTGGTCGCCATCAAGAAAGTATTTCAGGACACAGAGATTTAAGAAATCGAGAGCTCCAGATC 300
|||
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
|||
Db 301 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTCGGTTATTTCTTCTACTCCAGTGGT 360
|||
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
|||
Db 361 GAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACACAGTATAC 420
|||
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
|||
Db 421 AGAGTTGCCAGACACTATAGTCAGGACCAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480
|||
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
|||
Db 481 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAAATCTGCCATCGG 540
|||
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
|||
Db 541 GATATTAAACCCGAGAACCTCTTTGGTGGATCCCTGATACCTGTATTTAAAACTCTGTGAC 600
|||
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
|||
Db 601 TTTGGAAGTGCANAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCTCGG 660
|||
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
|||
Db 661 TACTATAGGCGCACAGAGTTGATCTTTGGAGCCACTGATATATACCTCTAGTATAGATGTA 720
|||
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
|||
Db 721 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTTACTAGGACCAACCAATATTTCCAGGGGAT 780
|||
QY 271 SerGlyValAspGlnLeuValGluIleIleLysVal 282
|||
Db 781 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTG 816
|||
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Search completed: September 18, 2006, 02:09:17  
Job time : 268 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2006, 00:35:50 ; Search time 5832 Seconds  
(without alignments)  
6480.268 Million cell updates/sec

Title: US-10-733-816-2  
Perfect score: 2081  
Sequence: 1 MEYMPMEGGMGRPTTSP.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/abs/ABSSWEB.spool/US10733816/runat.15092006.085444.15467/app.query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p  
-USER=US10733816 @CGN 1.1 8328 @runat.15092006.085444.15467 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	2024	97.3	1389	2 AR262205 Sequence
2	2024	97.3	1389	2 AR270851 Sequence
3	2024	97.3	1389	2 AX777402 Sequence

4	2024	97.3	1389	5 HUMGLSYKIN	L33801 Human prote
5	2015	96.8	1525	6 RNTAU	AF156099 Mus muscu
6	2015	96.8	1535	6 AF156099	AR059074 Sequence
7	2015	96.8	1972	2 AR059074	AR097211 Sequence
8	2015	96.8	1972	2 AR097211	BD181611 Method of
9	2015	96.8	1972	2 BD181611	E08007 DNA encodin
10	2015	96.8	1972	2 E08007	BC0060743 Mus muscu
11	2015	96.8	2841	6 BC0060743	AB066114 Mus muscu
12	2015	96.8	8304	6 AB066114	AX821914 Sequence
13	2013	96.7	1231	2 AX821914	AX701656 Sequence
14	2013	96.7	1263	5 AX701656	CR536510 Homo sapi
15	2013	96.7	1263	5 CR536510	AX701653 Sequence
16	2013	96.7	1389	2 AX701653	BC006936 Mus muscu
17	2013	96.7	1503	6 BC006936	BC012760 Homo sapi
18	2013	96.7	1815	2 BC012760	BC012760 Homo sapi
19	2013	96.7	2374	5 BC012760	53428 Rat mRNA fo
20	2012	96.7	1474	6 RNSK3B	AR059073 Sequence
21	2010	96.6	2088	2 AR059073	AR097210 Sequence
22	2010	96.6	2088	2 AR097210	E08052 cDNA encodi
23	2010	96.6	2088	2 E08052	AY392021 Spermophi
24	2008	96.5	1437	6 AY392021	AY335634 Synthetic
25	1996.5	95.9	1302	8 AY335634	CQ986514 Sequence
26	1996.5	95.9	1639	2 CQ986514	CQ981289 Sequence
27	1996.5	95.9	1639	2 CQ981289	CS160757 Sequence
28	1996.5	95.9	1639	2 CS160757	BC000251 Homo sapi
29	1996.5	95.9	1639	5 BC000251	AB032265 Danio rer
30	1959	94.1	2321	11 AB032265	AJ223502 Danio rer
31	1959	94.1	2624	11 AJ223502	L38492 Xenopus lae
32	1931	92.8	4394	11 XELGSK	BC108581 Xenopus l
33	1931	92.8	2090	11 BC108581	U31862 Xenopus lae
34	1923	92.4	1263	11 U31862	AJ223501 Danio rer
35	1704.5	81.9	2983	11 DAR223501	BC056332 Danio rer
36	1704.5	81.9	3040	11 BC056332	BC059552 Danio rer
37	1704.5	81.9	3100	11 BC059552	AB032264 Danio rer
38	1669.5	80.2	2949	11 AB032264	AK173391 Clona int
39	1669.5	80.1	1939	13 AK173391	AB031544 Clona int
40	1666.5	80.1	2708	13 AB031544	AB211133 Clona int
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42	1663	79.9	1027	2 CQ719548	DD210782 KINASES A
43	1634.5	78.5	1698	2 DD210782	AV624076 Lytechinu
44	1632	78.4	1245	13 AV624076	AJ222641 Paracentr
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ALIGNMENTS

RESULT 1	AR262205	AR262205	Sequence 3 from patent US 6323029.	1389 bp	DNA	linear	PAT 29-JAN-2003
LOCUS	AR262205	AR262205	Sequence 3 from patent US 6323029.	1389 bp	DNA	linear	PAT 29-JAN-2003
DEFINITION	AR262205	AR262205	Sequence 3 from patent US 6323029.	1389 bp	DNA	linear	PAT 29-JAN-2003
ACCESSION	AR262205	AR262205	Sequence 3 from patent US 6323029.	1389 bp	DNA	linear	PAT 29-JAN-2003
VERSION	AR262205.1	AR262205.1	GI:28073593	1389 bp	DNA	linear	PAT 29-JAN-2003
KEYWORDS	AR262205.1	AR262205.1	GI:28073593	1389 bp	DNA	linear	PAT 29-JAN-2003
SOURCE	Unknown.	Unknown.	Unknown.	1389 bp	DNA	linear	PAT 29-JAN-2003
ORGANISM	Unknown.	Unknown.	Unknown.	1389 bp	DNA	linear	PAT 29-JAN-2003
REFERENCE	1	1	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
AUTHORS	Butler, M.M., McKay, R., Monia, B.P. and Wyatt, J.	Butler, M.M., McKay, R., Monia, B.P. and Wyatt, J.	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
TITLE	Antisense modulation of glycogen synthase kinase 3 beta expression	Antisense modulation of glycogen synthase kinase 3 beta expression	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
JOURNAL	Patent: US 6323029-A 3 27-NOV-2001.	Patent: US 6323029-A 3 27-NOV-2001.	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
FEATURES	Location/Qualifiers	Location/Qualifiers	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
source	1. 1389	1. 1389	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
ORIGIN	/organism="unknown"	/organism="unknown"	(bases 1 to 1389)	1389 bp	DNA	linear	PAT 29-JAN-2003
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Db 40 ATGTCAGGCGCGCCAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGTCAGCAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGCAAGACGCGCAGCAAGGTGACACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70
Db 160 GTGGCAACTCTCGGCAAGGTTCAGACAGCGCCACAGAGTCAAGATCCAGACACTAAA 219
Qy 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCCAGGAGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAenArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGTATTGTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPheThrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCATCTGTAAACATAGTCGGATTGCTTCTTCTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATATC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCACAGACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGATCAGCTGTTCCGAAGTTTAGCTTATATCCATTCCTTTGGAAATCTGCCATCGG 579
Qy 191 AspIleLysProGlnAenLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGACCTCTTGTGATCCTGTACTGCTGTATTAAAACTCTGTGAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAenValSerTyrIleCysSerArg 230
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Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGATCATGTTGGTAGAAATAATCAAGGTCCTGGGAATCCCAACAGGGAGCAA 879
Qy 291 IleArgGluMetAenProAenTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
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Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
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Qy 351 AspGluLeuArgAspProAenValLysHisProAenGlyArgAspThrProAlaLeuPhe 370
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Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191
RESULT 2
LOCUS AR270851 1389 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1414 from patent US 6500938.
ACCESSION AR270851
VERSION AR270851.1 GI:29702085
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1389)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1414 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
WOX;
FEATURES
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Location/Qualifiers
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Alignment Scores: 1.51e-184 Length: 1389
Pred. No.: 2024.00 Matches: 384
Score: 2024.00 Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
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DB: 2
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Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTCAGGCGCGCCAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGTCAGCAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGCAAGACGCGCAGCAAGGTGACACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70
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Qy 111 MetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPheThrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCATCTGTAAACATAGTCGGATTGCTTCTTCTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATATC 459
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Qy 391 HisAlaArgile 394

Db 1180 CATGCTCGGATT 1191

RESULT 5

RNTAU 1525 bp mRNA linear ROD 18-APR-2005

LOCUS R. norvegicus mRNA for tau protein kinase I.

DEFINITION X73653.6 S63460

ACCESSION X73653.1 GI:402651

VERSION tau protein kinase.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 1525)

AUTHORS Ishiguro, K., Shiratsuchi, A., Sato, S., Omori, A., Arioka, M., Kobayashi, S., Uchida, T. and Imahori, K.

TITLE Glycogen synthase kinase 3 beta is identical to tau protein kinase I generating several epitopes of paired helical filaments

JOURNAL FEBS Lett. 325 (3), 167-172 (1993)

PUBMED 7686508

REFERENCE 2 (bases 1 to 1525)

AUTHORS Kobayashi, S., Ishiguro, K., Omori, A., Takamatsu, M., Arioka, M., Imahori, K. and Uchida, T.

TITLE A cdc2-related kinase PSSALRE/cdk5 is homologous with the 30 kDa subunit of tau protein kinase II, a proline-directed protein kinase associated with microtubule

JOURNAL FEBS Lett. 335 (2), 171-175 (1993)

PUBMED 8253190

REFERENCE 3 (bases 1 to 1525)

AUTHORS Uchida, T.

TITLE Direct Submission

JOURNAL Submitted (17-AUG-1993) T. Uchida, Mitsuishi Kasei, Institute of Life Sciences, 11 Minamiooya Machida-shi, Tokyo 194, JAPAN

COMMENT On May 10, 2005 this sequence version replaced gi:393351.

FEATURES

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Alignment Scores:

Pred. No.: 1,25e-183 Length: 1525

Score: 2015.00 Matches: 386

Percent Similarity: 98.0% Conservative: 0

Best Local Similarity: 98.0% Mismatches: 2

Query Match: 96.8% Indels: 6

DB: Gaps: 1

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Db 110 GAAGGAAAGGTGAATCGAGAGAGCCATCATCTCGGGCGCGAGAACCACTCTCTTT 169

Qy 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40

Db 170 GCGGAGAGCTGCAAGCCAGTCGAGAGCCTTCAGCTTTGGTAGCATGAAGTTAGCAGA 229

Qy 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60

Db 230 GATAAAGATGGCAGCAAGGTAAACACAGCTGGTGGCAACTCTCGACAGGGTCTCTGACAG 289

Qy 61 ProGlnGluValSerTyrThrAspThrLysValLleGlyAsnGlySerPheGlyValVal 80

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Db 410 AAGCGATTAAAGAACCCAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTC 469

Qy 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140

Db 470 CGATTGCGGTATTCTTCTACTCGAGTGGCGAGAAAGATGAGGTCTACCTTAACCTG 529

Qy 141 ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys 160

Db 530 GTGCTGGAGTATGTTCCGGAAACAGTGTACAGAGTGCAGACACTATAGTCGAGCCAAG 589

Qy 161 GlnThrLeuProValLleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180

Db 590 CAGACACTCCCTGTGATCTATGTCAGTTCAGTGTATATGATACAGCTGTTCAGAACTAGCC 649

Qy 181 TyrIleHisSerPheGlyLleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200

Db 650 TATATCCATTCTCTGGGATCTGCCATCGAGACATTAACACAGAACCTCTTGTGCTGAT 709

Qy 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220

Db 710 CCTGATACAGCTGTATTAAACTCTCGGACTTTGGAGTGCNAAGCAGCTGGTCCGAGGA 769

Qy 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuLlePheGly 240

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Qy 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260

Db 830 GCCACCGATTACAGCTCTAGTAGATGATGCTGTCGAGGCTGTGTGTGGCTGAATG 889

Qy 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluLleIle 280

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Db      1217 CCAATGGGGGAGACACACCTGCACCTCTTCAACTTTACCACTCAAGAACTGTCAAGTAAC 1276
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DEFINITION Sequence 2 from patent US 5837853.
ACCESSION AR059074
VERSION    AR059074.1 GI:5984651
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1972)
AUTHORS    Takashima,A., Hoshino,T., Imahori,K., Saito,K.-i., Shiratsuchi,A.
TITLE      Preventive or therapeutic agents for alzheimers disease a screening
            method of alzheimers disease and tau-protein kinase I originated
            from human being
JOURNAL    Patent: US 5837853-A 2 17-NOV-1998;
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Pred. No.:      1.75e-183      Length:      1972
Score:          2015.00      Matches:      386
Percent Similarity: 98.0%      Conservative: 0
Best Local Similarity: 98.0%      Mismatches: 2
Query Match:    96.8%      Indels:      6
DB:             2      Gaps:      1

US-10-733-816-2 (1-394) x AR059074 (1-1972)

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Db      170 GCGGAGAGCTGCAAGCCAGTCGACGAGCCCTTCAGCTTTTGGTAGCATGAAGTTAGCAGA 229
Qy      41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
Db      230 GATAAAGTGGCAGCAGGTAAACACAGTGTGGCACTCTTGACAGGGTCTCTGACAGG 289
Qy      61 ProGlnGluValSerThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
Db      290 CCACAGGAAGTCAGTTACACAGACACTAAAGTCATTGGAAATGGGTCAATTTGGTGGTA 349
Qy      81 TyrGlnAlaIysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
Db      350 TATCAGGCACCAACTTTGTGACTCAGGAGAACCTGGTGGCCATCAAGAAAGTTCTTCAGGAC 409
Qy      101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
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Qy      121 ArgLeuArgThrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db      470 CGATTGCGGTATTTCTTCTACTCGAGTGGCGAGAAAGATGAGGTCTACCTTAACCTG 529
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Db      590 CAGACACTCCCTGTGTATCTATGTCAAGTTGTATATGTACAGCTGTTCAAGAGTCTAGCC 649
Qy      181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuLeuAsp 200
Db      650 TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAACCCAGAACCTCTTTCGTGGAT 709
Qy      201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
Db      710 CCTGATACAGCTGTATTAACACTCTCGACTTTTGGAAAGTGCAAGCAGCTGTCGAGGA 769
Qy      221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
Db      770 GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCCACAGAGCTGATCTTTGGA 829
Qy      241 AlaThrAspTyrThrSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
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Db      1070 CCAGAGGCAATCGCACTGTGTAGCCCTCTCTCGAGTACACGCCGACCCCGCTTAACA 1129
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Db      1190 CCAAAATGGGCGAGACACACTGCTCTTCAACTTTTACCACTCAAGAACTGTCAAGTAAC 1249
Qy      381 ProProLeuAlaThrIleLeuLeuProProHisAlaArgile 394
Db      1250 CCACCTCTGGCCACCACTCTTATCCCTCTCAGCTCGGATT 1291

RESULT 8
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LOCUS      AR097211      1972 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6071694.
ACCESSION AR097211
VERSION    AR097211.1 GI:12805941
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1972)
AUTHORS    Takashima,A., Hoshino,T., Imahori,K., Saito,K.-i., Shiratsuchi,A.
TITLE      Screening method for therapeutic agents against Alzheimer's disease
            and Sato,S.
JOURNAL    Patent: US 6071694-A 2 06-JUN-2000;
FEATURES   Location/Qualifiers
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Alignment Scores:      1.75e-183      Length:      1972
Pred. No.:

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Percent Similarity:   98.0%                Conservative:            0
Best Local Similarity: 98.0%                Mismatches:           2
Query Match:         96.8%                Indels:               6
DB:                  2                    Gaps:                 1

US-10-733-816-2 (1-394) x AR097211 (1-1972)

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QY      21  AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
Db      170 GCGAGAGCTGCAAGCAGCTTCAGCTTTGGTAGCATGAAGATTAGCAGA 229
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Db      530 GTGCTGGACTATGTTCCGGAACAGGTACAGAGTCCGACAGACATATAGTCGAGCCAG 589
QY      161 GlnThrLeuProValLileTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
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DEFINITION Method of the phosphorylation of tau protein.
ACCESSION  BD181611
VERSION    BD181611.1 GI:30792529
KEYWORDS   JP 2002335983-A/1.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
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REFERENCE  1 (bases 1 to 1972)
AUTHORS    Ishiguro,K., Sato,S., Uchida,Y. and Imahori,K.
TITLE      Method of the phosphorylation of tau protein
JOURNAL    Patent: JP 2002335983-A 1 26-NOV-2002;
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            PI KOICHI ISHIGURO, SHOBU SATO, YO UCHIDA, KAZUTOMO IMAHORI PC
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DB 710 CTTGATACAGCTGTATTAACCTCTGCGACTTTGGAGTGCAGAGCTGTGTCGAGGA 769
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ACCESSION E08007

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VERSION E08007.1 GI:2176138
KEYWORDS JP 1994239893-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 1972)
AUTHORS Ishiguro, K., Sato, N., Uchida, I. and Imahori, K.
TITLE PHOSPHORYLATION OF TAU PROTEIN
JOURNAL Patent: JP 1994239893-A 1 30-AUG-1994;
MITSUBISHI KASEI CORP
COMMENT OS Rattus sp. (rat)
PN JP 1994239893-A/1
PD 30-AUG-1994
PF 03-JUL-1992 JP 1992177241
PI ISHIGURO KOICHI, SATO NAOTAKE, UCHIDA ISAO, IMAHORI KAZUTOMO
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Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
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VERSION BC060743.1 GI:38511427  
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SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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1 (bases 1 to 2841)  
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Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Hoskins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
Schneringer, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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Strausberg, R.  
Direct Submission  
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Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-ehgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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QY	41	AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60	
Db	1543	GATAAGATGCGACGAGGTAAACACAGTAGTGGCACTCTCTGGCCAGGTCCTGCACAG 1602	
QY	61	ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80	
Db	1603	CCACAGAGTCAAGTTATACAGACACGAAAGTGAATTCGAAATGGATCATTTGGTGTGGTA 1662	
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QY	121	ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140	
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QY	141	ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys 160	
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QY	161	GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180	
Db	1903	CAGAGCTCCTGTGATCTATGTCAGTTGTATATGATCAGCTGTTCAAGAGTCTAGCC 1962	
QY	181	TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200	
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QY	221	GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240	
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QY	241	AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260	
Db	2143	GCCACTGATTACAGCTCCAGTATAGATGTATGTGCTCGAGCTGTGTGGTGGCTGAATTG 2202	
QY	261	LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle 280	
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QY	281	LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300	
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Db	2383	CCAGAGGCATTCGACTGTGCAGCCGCTGCTGAGGTACACACTACCGCCCGGCTAACCA 2442	
QY	341	ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360	
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QY	361	ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380	
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LOCUS		Mus musculus mRNA for glycogen synthase kinase 3 beta/tau protein	
DEFINITION		kinase I, complete cds.	
ACCESSION		AB066114	
VERSION		AB066114.1 GI:57834171	
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SOURCE		Mus musculus	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		Sano, Y., Nakano, A., Hirai, K., Ohta, S., Yanagisawa, M., Sato, S. and Imahori, K.	
TITLE		Glycogen synthase kinase 3b gene: complete genomic and cDNA structures	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 8304)	
AUTHORS		Sano, Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (13-JUL-2001) Yumiko Sano, National Institute of Advanced Industrial Science and Technology (AIST), Research Center for Glycoscience (RCG), Glycogene Function Team, Central-2 OSL, 1-1-1 Umezono, Tsukuba, Ibaraki, 305-8568, Japan	
FEATURES		[E-mail:yumiko-sano@aist.go.jp, Tel:81-29-861-3197, Fax:81-29-861-3191]	
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QY      61 ProGlnGluValSerThrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
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QY      141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
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QY      161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
Db      1975 CAGACACTCCTGTGTATCTATGCAAGTGTATATGTATATGATCAGCTGTTTCAGAAAGTCTAGCC 2034
QY      181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAnLeuLeuAsp 200
Db      2035 TATATCCATTCTTTGGAATCTGCATCGAGACATTAAACCAACAGAAACCTCTTTGTGGAT 2094
QY      201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValIleGly 220
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QY      221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
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QY      241 AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu 260
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DEFINITION Sequence 42 from Patent WO03068961.
ACCESSION AX821914
VERSION AX821914.1 GI:39725135
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
TITLE Method to modify differentiation of pluripotential stem cells
JOURNAL Patent: WO 03068961-A 42 21-AUG-2003;
Axordia Limited (GB)
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RESULT 14

AX701656

LOCUS

DEFINITION

AX701656 1263 bp DNA linear PAT 03-APR-2003  
Sequence 6 from Patent WO03000882.

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VERSION AX701656.1 GI:29537197
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Holder, J.C.
TITLE Transgenic models for glucose homeostasis comprising human gsk-3
JOURNAL Patent: WO 0300882-A 6 03-JAN-2003;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
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Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
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Db 1141 CATGCTCGGATT 1152

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CR536510
LOCUS
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stopcodon.
ACCESSION
CR536510.1 GI:49168505
VERSION
Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1263)
Hallack,A., Ebert,L., Mkundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
Unpublished
2 (bases 1 to 1263)
Hallack,A., Ebert,L., Mkundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
Direct Submission
JOURNAL
Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT
RZPD: RZPD0834A0920D, ORFNo 3071
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834A0920D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
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Contact: Inge Ariart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 100  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available from RZPD;  
contact RZPD (customer.service@rzpd.de) for further information.  
This CDS clone is a part of a collection of human full ORF clones  
jointly established and verified by the Harvard Institute of  
Proteomics and RZPD.

This CDS has been cloned incl. stopcodon.  
The CDS has been inserted into pDONR201 via a BP Clonase(TM)  
reaction. Additional sequence has been added in front of the start  
codon: att. .AAAAAA GCA GGC TCC ACC (ARG).

The stopcodon is followed by the 3' att site:  
(stop)GACCCAGCTTCTT. att Compared to the reference sequence  
BC012760

we did not find any amino acid exchanges.

Clone distribution: <http://www.rzpd.de/products/orfclones/>.

#### FEATURES

##### source

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##### ORIGIN

Alignment Scores:					
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Score:	2013.00	Matches:	383		
Percent Similarity:	99.7%	Conservative:	0		
Best Local Similarity:	99.7%	Mismatches:	1		
Query Match:	96.7%	Indels:	0		
DB:	5	Gaps:	0		
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Qy 31 SerAlaPheGlySerMetLysValSerAtqAspLysAspGlySerLysValThrThrVal 50					
Db 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGACCGCAGCAGCAGCAGCAGTG 120					
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Db 121 GTGGCACTCTCTGGCAGCGGTCCAGACAGCCCAAGAACTCAGCTATACAGACACTAA 180					
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90					
Db 181 GTGATTGGAATGATCATTTGGTGGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 240					
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110					

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Qy      211  |||||PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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Qy      231  |||||TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db      661  |||||TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGA 720
Qy      251  |||||TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db      721  |||||TGCTCTGCTGGCTGTGTGGCTGAGCTGTTACTAGGACAAACCAATATTTCCAGGGGAT 780
Qy      271  |||||SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
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Qy      351  |||||AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370
Db      1021  |||||GATGATTTACGGACCCCAATGTCAAACTACAAATGGGGGAGACACACCTGCACCTCTC 1080
Qy      371  |||||AsnPheThrThrGlnLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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Search completed: September 18, 2006, 02:18:35  
Job time : 5862 secs



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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2006, 17:25:11 ; Search time 34 Seconds  
(without alignments)  
818.678 Million cell updates/sec

Title: US-10-733-816-2  
Perfect score: 2081  
Sequence: 1 MEYMPMEGGMSGRPTTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2081	100.0	394	6	US-10-733-816-2
2	2024	97.3	420	6	US-10-733-816-1
3	2013	96.7	420	7	US-11-299-324-10
4	1996.5	95.9	433	7	US-11-299-324-15
5	1996.5	95.9	433	7	US-11-283-329-216
6	1919	92.2	387	7	US-11-299-324-18
7	1883.5	90.5	361	6	US-10-733-816-3
8	1808	86.9	388	7	US-11-299-324-16
9	1609	77.3	447	6	US-10-733-816-5
10	1609	77.3	483	6	US-10-733-816-4
11	1609	77.3	483	6	US-10-553-520-85
12	1588	76.3	351	6	US-10-733-816-7
13	1588	76.3	387	6	US-10-733-816-6
14	1416	68.0	278	7	US-11-299-324-14
15	1283	61.7	399	7	US-11-056-3558-82944
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17	1278	61.4	401	6	US-10-449-902-51997
18	1276	61.3	378	7	US-11-056-3558-82945
19	1264.5	60.8	293	7	US-11-299-324-17
20	1263.5	60.7	424	6	US-10-449-902-48109
21	1258	60.5	429	7	US-11-056-3558-46581
22	1258	60.5	469	7	US-11-056-3558-46580
23	1258	60.5	472	7	US-11-056-3558-46579
24	1257	60.4	409	6	US-10-953-349-33014
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26	1257	60.4	428	6	US-10-953-349-33013	Sequence 33013, A
27	1257	60.4	428	7	US-11-056-3558-13203	Sequence 13203, A
28	1256	60.4	412	7	US-11-056-3558-4903	Sequence 4903, Ap
29	1256	60.4	448	7	US-11-056-3558-4902	Sequence 4902, Ap
30	1254.5	60.3	408	6	US-10-449-902-52659	Sequence 52659, A
31	1254	60.3	409	7	US-11-056-3558-4904	Sequence 4904, Ap
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35	1250.5	60.1	392	7	US-11-056-3558-5573	Sequence 5573, Ap
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37	1250.5	60.1	463	7	US-11-056-3558-5571	Sequence 5571, Ap
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40	1246	59.9	403	6	US-10-449-902-53848	Sequence 53848, A
41	1246	59.9	409	7	US-11-056-3558-33900	Sequence 33900, A
42	1246	59.9	409	7	US-11-056-3558-33900	Sequence 33900, A
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44	1246	59.9	409	7	US-11-056-3558-100020	Sequence 100020, A
45	1246	59.9	409	7	US-11-056-3558-111259	Sequence 111259, A

ALIGNMENTS

RESULT 1

US-10-733-816-2  
; Sequence 2, Application US/10733816  
; Publication No. US2006008932A1  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Coit, Doris G.  
; APPLICANT: Nguyen, Steve H.  
; APPLICANT: Medina-Seiby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/10733,816  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US/10/211,412  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US09/916,109  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-733-816-2

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Gaps	0;						
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Db	61	PQVSYTDTKVI	NGSFGVYVYQAKL	CDGSELVAIKK	VLQDKRFN	RLQIMR	LDCNIV 120
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Db	121	RLBYFFYSSEK	DEVYLNILVDY	VPETVYRVARH	YSRAKOTLP	VIYVKLYM	QLFSLA 180
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US-11-299-324-15

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Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

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61 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
131 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 190  
121 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 180  
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301 WTKDSSGTGHTSGVRFRTTPEAIALCSRLLEYTPTARLTPLACAHSAFFDELDPN 360  
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361 VKLPNGRDTPALNFTTQELSSNPPLATILIPPHARI 397

RESULT 6  
US-11-299-324-18  
; Sequence 18, Application US/11299324  
; Publication No. US20060127388A1  
; GENERAL INFORMATION:  
; APPLICANT: Cain, Michael  
; APPLICANT: Yaworsky, Paul J  
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof  
; FILE REFERENCE: WYE-052  
; CURRENT APPLICATION NUMBER: US/11/299,324  
; CURRENT FILING DATE: 2005-12-09  
; PRIOR APPLICATION NUMBER: US 60/634,813  
; PRIOR FILING DATE: 2004-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-299-324-18

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71 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 130  
61 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
131 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 190  
121 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 180  
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361 NFFTQDANT 369

US-11-283-329-216

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Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

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71 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 130  
61 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
131 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 190  
121 EKKDEVYLNLDVYPETVVRVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 180  
191 DIKPQNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
181 DIKPQNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
251 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTYEFKFPQIKAH 310  
241 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTYEFKFPQIKAH 300  
311 WTK-----VFRRPTTPEAIALCSRLLEYTPTARLTPLACAHSAFFDELDPN 357  
301 WTKDSSGTGHTSGVRFRTTPEAIALCSRLLEYTPTARLTPLACAHSAFFDELDPN 360  
358 VKHPNGRDTPALNFTTQELSSNPPLATILIPPHARI 394  
361 VKLPNGRDTPALNFTTQELSSNPPLATILIPPHARI 397

RESULT 5  
US-11-283-329-216  
; Sequence 216, Application US/11283329  
; Publication No. US20060134670A1  
; GENERAL INFORMATION:  
; APPLICANT: Piu, Fabrice  
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR  
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS  
; FILE REFERENCE: ACADIA 043A  
; CURRENT APPLICATION NUMBER: US/11/283,329  
; CURRENT FILING DATE: 2005-11-18  
; PRIOR APPLICATION NUMBER: 60/629,811  
; PRIOR FILING DATE: 2004-11-19  
; NUMBER OF SEQ ID NOS: 242  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 216  
; LENGTH: 433  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-283-329-216

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Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

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71 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 130  
61 VINGSGFVVYQAKLDCSGLVIAKKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
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## RESULT 7

US-10-733-816-3  
 ; Sequence 3, Application US/10733816  
 ; Publication No. US20060088932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harrison, Stephen D.  
 ; APPLICANT: Hall, John A.  
 ; APPLICANT: Calderon-Cacia, Maria  
 ; APPLICANT: Zhong, Ziyang  
 ; APPLICANT: Fang, Eric Y.  
 ; APPLICANT: Coit, Doris G.  
 ; APPLICANT: Nguyen, Steve H.  
 ; APPLICANT: Medina-Selby, Angelica  
 ; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
 ; FILE REFERENCE: 59516-162/PP-15876.002/200130.524  
 ; CURRENT APPLICATION NUMBER: US/10/733.816  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: US/10/211.412  
 ; PRIOR FILING DATE: 2002-07-31  
 ; PRIOR APPLICATION NUMBER: US09/916,109  
 ; PRIOR FILING DATE: 2001-07-25  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 361  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-733-816-3

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 QY 1 MEYMPGGMGGRPTTSFAESCKPVQPSAFGSMKVS RDKQSKVTTTVA TPQGQPD 60  
 DB 1 MEYMPGGMG-----GSKVTTTVA TPQGQPD 27  
 QY 61 PQSVSYTDTKVI GNGSGVYVYQAKL CDSGELVAIKKVLQDKRPNRELOIMRKL DHCNIV 120  
 DB 28 PQSVSYTDTKVI GNGSGVYVYQAKL CDSGELVAIKKVLQDKRPNRELOIMRKL DHCNIV 87  
 QY 121 RLRYFFYSSEKKEDEVYLNLDVYVPTVTVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180  
 DB 88 RLRYFFYSSEKKEDEVYLNLDVYVPTVTVARHYSRAKQTLPIVYVKLYMYQLFRSLA 147  
 QY 181 YIHSFGICHRDIKPNLLDPDTAVLKLCDFGSAKQLV RGEPNVSYICSRYRAP ELIFG 240  
 DB 148 YIHSFGICHRDIKPNLLDPDTAVLKLCDFGSAKQLV RGEPNVSYICSRYRAP ELIFG 207  
 QY 241 ATDYTSSIDVMSAGCVLAELLGQPIPGDSGVDQVLEI IKVLGTPTRQIREMNP NYTE 300  
 DB 208 ATDYTSSIDVMSAGCVLAELLGQPIPGDSGVDQVLEI IKVLGTPTRQIREMNP NYTE 267  
 QY 301 FKPPQIKAHPTWKVFRPRTPEALCSRLLEYTP TARTLPLECAHSFFDEL RDPNVKH 360  
 DB 268 FKPPQIKAHPTWKVFRPRTPEALCSRLLEYTP TARTLPLECAHSFFDEL RDPNVKH 327  
 QY 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394  
 DB 328 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 361

## RESULT 8

US-11-299-324-16  
 ; Sequence 16, Application US/11299324  
 ; Publication No. US20060127388A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cain, Michael  
 ; APPLICANT: Yaworsky, Paul J  
 ; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof  
 ; FILE REFERENCE: WYE-052  
 ; CURRENT APPLICATION NUMBER: US/11/299,324  
 ; CURRENT FILING DATE: 2005-12-09

; PRIOR APPLICATION NUMBER: US 60/634,813  
 ; PRIOR FILING DATE: 2004-12-10  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 16  
 ; LENGTH: 388  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-299-324-16

Query Match 86.9%; Score 1808; DB 7; Length 388;  
 Best Local Similarity 91.4%; Pred. No. 2.1e-105;  
 Matches 351; Conservative 0; Mismatches 1; Indels 32; Gaps 1;  
 QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVS RDKQSKVTTTVA TPQGQPD RPQSVSYTDTK 70  
 DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVS RDKQSKVTTTVA TPQGQPD RPQSVSYTDTK 60  
 QY 71 VI GNGSGFVYVYQAKL CDSGELVAIKKVLQDKRPNRELOIMRKL DHCNIVRLRYFFVSSG 130  
 DB 61 VI GNGSGFVYVYQAKL CDSGELVAIKKVLQDKRPNRELOIMRKL DHCNIVRLRYFFVSSG 120  
 QY 131 EKKDEVYLNLDVYVPTVTVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190  
 DB 121 EKKDEVYLNLDVYVPTVTVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180  
 QY 191 DIKPNLLDPDTAVLKLCDFGSAKQLV RGEPNVSYICSRYRAP ELIFGATDYTSSIDV 250  
 DB 181 DIKPNLLDPDTAVLKLCDFGSAKQLV RGEPNVSYICSRYRAP ELIFGATDYTSSIDV 240  
 QY 251 WSAGCVLAELLGQPIPGDSGVDQVLEI IKVLGTPTRQIREMNP NYTEFKPPQIKAH 310  
 DB 241 WSAGCVLAELLGQPIPGDSGVDQVLEI IKVLGTPTRQIREMNP NYTEFKPPQIKAH 270  
 QY 311 WTKVFRPRTPEALCSRLLEYTP TARTLPLECAHSFFDEL RDPNVKH PNRGRTPALF 370  
 DB 271 --KVPRTPEALCSRLLEYTP TARTLPLECAHSFFDEL RDPNVKH PNRGRTPALF 328  
 QY 371 NFTTQELSSNPPLATILIPPHARI 394  
 DB 329 NFTTQELSSNPPLATILIPPHARI 352

## RESULT 9

US-10-733-816-5  
 ; Sequence 5, Application US/10733816  
 ; Publication No. US20060088932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harrison, Stephen D.  
 ; APPLICANT: Hall, John A.  
 ; APPLICANT: Calderon-Cacia, Maria  
 ; APPLICANT: Zhong, Ziyang  
 ; APPLICANT: Fang, Eric Y.  
 ; APPLICANT: Coit, Doris G.  
 ; APPLICANT: Nguyen, Steve H.  
 ; APPLICANT: Medina-Selby, Angelica  
 ; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
 ; FILE REFERENCE: 59516-162/PP-15876.002/200130.524  
 ; CURRENT APPLICATION NUMBER: US/10/733.816  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: US/10/211.412  
 ; PRIOR FILING DATE: 2002-07-31  
 ; PRIOR APPLICATION NUMBER: US09/916,109  
 ; PRIOR FILING DATE: 2001-07-25  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 447  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-733-816-5

Query Match 77.3%; Score 1609; DB 6; Length 447;

Best Local Similarity 80.6%; Pred. No. 5.6e-93;  
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFGSMKVRDRDGGSKVTTTVAATPGGPPRPOEVS 66  
DB 73 GGGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119

QY 67 TDTKVIENGSGVYVYQAKLDCSGLVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 126  
DB 120 TDIKVIENGSGVYVYQARLAETRELVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 179

QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186  
DB 180 YSSGEKKDEVLYNLVLEYPTVTVRVARHFTKAKLTIPILYKVMYQLFRSLAYIHSOG 239

QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 246  
DB 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 299

QY 247 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306  
DB 300 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359

QY 307 KAHPTWKVFRPRTPPPAIALCSLLEYTPARLTPLCAHSAHSPFDELRODNVXHPNGRDT 366  
DB 360 KAHPTWKVFKSRTPPPAIALCSLLEYTPSSRLSPLEACAHSAHSPFDELRLCLGTQLPNNRPL 419

QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393  
DB 420 PPLFNFSAGELSLOPSNAILIPPHLR 446

## RESULT 10

US-10-733-816-4  
; Sequence 4, Application US/10733816  
; Publication No. US20060088932A1  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Coit, Doris G.  
; APPLICANT: Nguyen, Steve H.  
; APPLICANT: Medina-Selby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/10733,816  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US/10/211,412  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US09/916,109  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-733-816-4

Query Match 77.3%; Score 1609; DB 6; Length 483;  
Best Local Similarity 80.6%; Pred. No. 6e-93;  
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFGSMKVRDRDGGSKVTTTVAATPGGPPRPOEVS 66  
DB 73 GGGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119

QY 67 TDTKVIENGSGVYVYQAKLDCSGLVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 126  
DB 120 TDIKVIENGSGVYVYQARLAETRELVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 179

QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186  
DB 180 YSSGEKKDEVLYNLVLEYPTVTVRVARHFTKAKLTIPILYKVMYQLFRSLAYIHSOG 239

QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 246  
DB 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 299

QY 247 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306  
DB 300 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359

QY 307 KAHPTWKVFRPRTPPPAIALCSLLEYTPARLTPLCAHSAHSPFDELRODNVXHPNGRDT 366  
DB 360 KAHPTWKVFKSRTPPPAIALCSLLEYTPSSRLSPLEACAHSAHSPFDELRLCLGTQLPNNRPL 419

QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393  
DB 420 PPLFNFSAGELSLOPSNAILIPPHLR 446

## RESULT 11

US-10-553-520-85  
; Sequence 85, Application US/10553520  
; Publication No. US20060198885A1  
; GENERAL INFORMATION:  
; APPLICANT: Bodian, Dale  
; APPLICANT: Daouti, Sherif  
; APPLICANT: Kumar, Chandrika  
; APPLICANT: Latario, Brian  
; APPLICANT: Quintavalla, Joseph  
; TITLE OF INVENTION: High throughput functional genomic  
; FILE REFERENCE: 4-33178  
; CURRENT APPLICATION NUMBER: US/10/553,520  
; PRIOR FILING DATE: 2005-10-14  
; PRIOR APPLICATION NUMBER: 60/463,933  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-553-520-85

Query Match 77.3%; Score 1609; DB 6; Length 483;  
Best Local Similarity 80.6%; Pred. No. 6e-93;  
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFGSMKVRDRDGGSKVTTTVAATPGGPPRPOEVS 66  
DB 73 GGGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119

QY 67 TDTKVIENGSGVYVYQAKLDCSGLVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 126  
DB 120 TDIKVIENGSGVYVYQARLAETRELVAIKKVLQDKRFKRELQIMRKLHCNIVRLRYFF 179

QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186  
DB 180 YSSGEKKDEVLYNLVLEYPTVTVRVARHFTKAKLTIPILYKVMYQLFRSLAYIHSOG 239

QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 246  
DB 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIIFGATDYS 299

QY 247 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306  
DB 300 SIDVWSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359

QY 307 KAHPTWKVFRPRTPPPAIALCSLLEYTPARLTPLCAHSAHSPFDELRODNVXHPNGRDT 366  
DB 360 KAHPTWKVFKSRTPPPAIALCSLLEYTPSSRLSPLEACAHSAHSPFDELRLCLGTQLPNNRPL 419



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QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLENFSAGELSIQPSLNAILIPPHLR 446

RESULT 12
US-10-733-816-7
; Sequence 7, Application US/10733816
; Publication No. US2006008932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-7

Query Match 76.3%; Score 1588; DB 6; Length 351;
Best Local Similarity 86.2%; Pred. No. 8.8e-92;
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 46 KVTTVATPGQGPDRPQEVSYTDTKVIGNSFGVYQAKLSDGELVAIKKVLQDKRFKN 105
Db 3 KVTTVATLGGPERSQEVAYTDIKVIGNSFGVYQARLAETRELVAIKKVLQDKRFKN 62

QY 106 RELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVPETVYRVARHYSRAKOTLPV 165
Db 63 RELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVPETVYRVARHFTKAKUTPI 122

QY 166 IYVKLYMYQLFRSLAYTHSFGICHRDIKPNQLLLDPTAVLKLCDFGSAKQLVRGPNVS 225
Db 123 LYVKVYMYQLFRSLAYTHSFGVCHRDIKPNQLLLVDPDTAVLKLCDFGSAKQLVRGPNVS 182

QY 226 YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLGQPIFFPGDSGVQDLVEIIVLGT 285
Db 183 YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLGQPIFFPGDSGVQDLVEIIVLGT 242

QY 286 PTREQIREMNPNTPEKFPQIKAHPTWKVFRPTPEALCSRLLEYTPTARLTPLEAC 345
Db 243 PTREQIREMNPNTPEKFPQIKAHPTWKVFRPTPEALCSRLLEYTPTSSRLSPLAC 302

QY 346 AHSFFDELDRPNVKNHGRDTPALFNFTTQELSSNPPLATILIPPHAR 393
Db 303 AHSFFDELRCGLTQLPNNRPLPLPPLNFSAGELSIQPSLNAILIPPHLR 350

RESULT 14
US-11-299-324-14
; Sequence 14, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variance of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 14
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-299-324-14

Query Match 68.0%; Score 1416; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 3.4e-81;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 MSGRPRTTSPAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKDEVYLNLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIRPONLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIRPONLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIKV 282
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIKV 272
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## RESULT 15

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US-11-056-355B-82944
; Sequence 82944, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82944
; LENGTH: 399
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(399)
; OTHER INFORMATION: Ceres Seq. ID no. 12668003
US-11-056-355B-82944
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Query Match 61.7%; Score 1283; DB 7; Length 399;

Best Local Similarity 65.8%; Pred. No. 8.9e-73;

Matches 248; Conservative 49; Mismatches 66; Indels 14; Gaps 6;

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QY 30 PSAFGSMKVSRRDK-----DGSKVTT---VWATPGQGPDRP-QEVSYTDTKVIGNSFG 78
Db 16 PEGINEMKIKDDKEMEAUVDDGNGTETGHIIVTTIGKNCQPKQTISYMAERIVGQGSFG 75
QY 79 VYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYGKQDEVL 138
Db 76 IVFOAKCLETGETVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYGKQDEVL 134
QY 139 NLVLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHRDIKPNL 197
Db 135 NLVLEYVPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHRDIKPNL 194
QY 198 LLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVL 257
Db 195 LVNPHQVAKLDCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVL 254
QY 258 AELLGQPIFPDGSVDQVLEIKVLTPTREIQIREMKNPNYTEFKFPQIKAHFWTKVFRP 317
Db 255 AELLGQPLFPDGSVDQVLEIKVLTPTREIKCMNPNYTEFKFPQIKAHFWTKVFRP 314
QY 318 RTPPEALCSRLLPYTPARTLPLECAHSFPDELDDPNVKHPNGRDTFALFNFTTQEL 377
Db 318 RTPPEALCSRLLPYTPARTLPLECAHSFPDELDDPNVKHPNGRDTFALFNFTTQEL 377
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Db 315 RTPPEAVDLVSRLLQYSPNLRSTAMEAIVHPPFDELDDPNTRLPNGRALPPLFNFKPQEL 374
QY 378 -SSNPPLATILIPPHAR 393
Db 375 KGASLELLSKLIPDHAR 391
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2006, 17:24:21 ; Search time 183 Seconds  
(without alignments)  
997.304 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

Sequence: 1 MEYMPMEGGMGSRPRTTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.Main.\*  
1: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	3	US-09-916-109-2
2	2081	100.0	394	4	US-10-211-412A-2
3	2081	100.0	394	5	US-10-689-461-2
4	2024	97.3	420	3	US-09-916-109-1
5	2024	97.3	420	4	US-10-211-412A-1
6	2024	97.3	420	4	US-10-278-759-7
7	2024	97.3	420	5	US-10-482-524-4
8	2024	97.3	420	5	US-10-772-536-72
9	2024	97.3	420	5	US-10-689-461-1
10	2024	97.3	420	5	US-10-840-060-257
11	2024	97.3	420	6	US-11-288-493-72
12	2013	96.7	414	4	US-10-746-545-31
13	2013	96.7	420	4	US-10-278-759-6
14	2013	96.7	420	4	US-10-135-255-1
15	2013	96.7	420	4	US-10-746-545-15
16	2013	96.6	420	4	US-10-746-545-18
17	2010	96.6	420	4	US-10-278-759-2
18	2010	96.6	420	4	US-10-322-153A-1
19	2010	96.6	420	4	US-10-613-728-8
20	1997	96.0	385	4	US-10-684-421-53
21	1997	96.0	385	5	US-10-941-635-53
22	1996.5	95.9	433	4	US-10-278-759-8
23	1996.5	95.9	433	4	US-10-278-759-14
24	1996.5	95.9	433	4	US-10-302-812-62
25	1996.5	95.9	433	4	US-10-408-765A-1360
26	1996.5	95.9	433	5	US-10-828-669-5
27	1996.5	95.9	433	5	US-10-770-726-65

28	1883.5	90.5	361	3	US-09-916-109-3	Sequence 3, Appli
29	1883.5	90.5	361	4	US-10-211-412A-3	Sequence 3, Appli
30	1883.5	90.5	361	5	US-10-689-461-3	Sequence 3, Appli
31	1877	90.2	367	4	US-10-746-545-32	Sequence 32, Appli
32	1872.5	90.0	361	4	US-10-450-422-1	Sequence 1, Appli
33	1817	87.3	352	4	US-10-564-421-31	Sequence 31, Appli
34	1817	87.3	352	4	US-10-746-545-16	Sequence 16, Appli
35	1817	87.3	352	4	US-10-746-545-17	Sequence 17, Appli
36	1817	87.3	352	5	US-10-941-635-31	Sequence 17, Appli
37	1817	87.3	352	6	US-11-021-951-167	Sequence 167, App
38	1803	86.6	350	4	US-10-746-545-27	Sequence 27, Appli
39	1666.5	80.1	407	5	US-10-732-923-1457	Sequence 1457, Ap
40	1834.5	78.5	428	5	US-10-491-467-13	Sequence 13, Appli
41	1609	77.3	447	3	US-09-916-109-5	Sequence 5, Appli
42	1609	77.3	447	4	US-10-211-412A-5	Sequence 5, Appli
43	1609	77.3	447	5	US-10-689-461-5	Sequence 5, Appli
44	1609	77.3	483	3	US-09-916-109-4	Sequence 4, Appli
45	1609	77.3	483	4	US-10-211-412A-4	Sequence 4, Appli

## ALIGNMENTS

### RESULT 1

US-09-916-109-2

; Sequence 2, Application US/09916109

; Patent No. US20020082408A1

; GENERAL INFORMATION:

; APPLICANT: Harrison, Stephen D.

; APPLICANT: Hall, John A.

; APPLICANT: Calderon-Cacia, Maria

; APPLICANT: Zhong, Ziyang

; APPLICANT: Fang, Eric Y.

; APPLICANT: Coit, Doris G.

; APPLICANT: Nguyen, Steve H.

; APPLICANT: Medina-Selby, Angelica

; TITLE OF INVENTION: GSK3 POLYPEPTIDES

; FILE REFERENCE: PP-15876.002/200130.524

; CURRENT APPLICATION NUMBER: US/09/916,109

; CURRENT FILING DATE: 2001-07-25

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 394

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-916-109-2

Query Match 100.0%; Score 2081; DB 3; Length 394;

Best Local Similarity 100.0%; Pred. No. 3.7e-169;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEYMPMEGGMGSRPRTTSFAESCKPVQOPSAGSMKVS RDKGSKVTTVVATPGQCPDR	60
Db	1	MEYMPMEGGMGSRPRTTSFAESCKPVQOPSAGSMKVS RDKGSKVTTVVATPGQCPDR	60
Qy	61	PQVSYTDTKVI GNGSFGVYVYQAKL CDSGELVAIKKVLQDKR FKNRELQIMRKL DHCNIV	120
Db	61	PQVSYTDTKVI GNGSFGVYVYQAKL CDSGELVAIKKVLQDKR FKNRELQIMRKL DHCNIV	120
Qy	121	RLRYFFYSSEKKEDEVYLVNLDVVPETVTVRAHYSRAKQTLFVIVYKLYMYQLFSLA	180
Db	121	RLRYFFYSSEKKEDEVYLVNLDVVPETVTVRAHYSRAKQTLFVIVYKLYMYQLFSLA	180
Qy	181	YIHSFGICHRDIKPQNLLDPDPTAVLKLCDFGSAKQLVRGEPNNVYICSRYYRAPELIFG	240
Db	181	YIHSFGICHRDIKPQNLLDPDPTAVLKLCDFGSAKQLVRGEPNNVYICSRYYRAPELIFG	240
Qy	241	ATDTSSIDVWSAGCVLAELLLGQIPFGDSGDVQLVEIIVKVLGTPPTREQIRENNPNYTE	300
Db	241	ATDTSSIDVWSAGCVLAELLLGQIPFGDSGDVQLVEIIVKVLGTPPTREQIRENNPNYTE	300
Qy	301	FKFPQIKAHPTWKVFRPRTPEPAIALCSRLLEVTPTARLTPL ECAHSFFDEL RDPNVKH	360

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Db 301 FKFPQIKAHPTWKVFRPRTPEAIALCSRLLVTTPTARLTPLACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394

RESULT 2
US-10-211-412A-2
; Sequence 2, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/200130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-2

Query Match 100.0%; Score 2081; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.7e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQPD 60
Db 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQPD 60
QY 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
Db 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
QY 121 RLRYFFYSGEKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Db 121 RLRYFFYSGEKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
QY 181 YHISFGICHRDIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFG 240
Db 181 YHISFGICHRDIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFG 240
QY 241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTPTTREQIREMNPYTE 300
Db 241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTPTTREQIREMNPYTE 300
QY 301 FKFPQIKAHPTWKVFRPRTPEAIALCSRLLVTTPTARLTPLACAHSPFDELDPNVKH 360
Db 301 FKFPQIKAHPTWKVFRPRTPEAIALCSRLLVTTPTARLTPLACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394

RESULT 3
US-10-689-461-2
; Sequence 2, Application US/10689461
; Publication No. US2005004851A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
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; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/689,461
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-461-2

Query Match 100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.7e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQPD 60
Db 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQPD 60
QY 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
Db 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
QY 121 RLRYFFYSGEKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Db 121 RLRYFFYSGEKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
QY 181 YHISFGICHRDIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFG 240
Db 181 YHISFGICHRDIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFG 240
QY 241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTPTTREQIREMNPYTE 300
Db 241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTPTTREQIREMNPYTE 300
QY 301 FKFPQIKAHPTWKVFRPRTPEAIALCSRLLVTTPTARLTPLACAHSPFDELDPNVKH 360
Db 301 FKFPQIKAHPTWKVFRPRTPEAIALCSRLLVTTPTARLTPLACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFNTTQELSSNPPLATILIPPHARI 394

RESULT 4
US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. US20020082408A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-1

Query Match          97.3%; Score 2024; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 120

QY 131 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 240

QY 251 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQBELSSNPPLATILIPPHARI 394
Db 361 NFFTQBELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412A-1
; Sequence 1, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/2001130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-1

Query Match          97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 120

QY 131 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 240

QY 251 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQBELSSNPPLATILIPPHARI 394
Db 361 NFFTQBELSSNPPLATILIPPHARI 384

RESULT 6
US-10-278-759-7
; Sequence 7, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278.759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-278-759-7

Query Match          97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTSAESCCKPVQQPSAFGSMKVS RDKGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELOIMRKLDHCNI VRLRYFFYSSG 120

QY 131 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLLDPTDAVLKCLDFGSAKOLVRGEPNVSICYRYRAPELIFGATDYTSSIDV 240

QY 251 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAIACLSRLLEYTPPTARLTPLEACAHSFFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQBELSSNPPLATILIPPHARI 394
Db 361 NFFTQBELSSNPPLATILIPPHARI 384
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Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
Db 361 NFFTQELSSNPPLATILIPPHARI 384  
RESULT 7  
US-10-482-524-4  
; Sequence 4, Application US/10482524  
; Publication No. US20040261137A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithkline Beecham PLC  
; APPLICANT: Holder, Julie C  
; TITLE OF INVENTION: Models for Metabolic Disorders  
; FILE REFERENCE: PG4458  
; CURRENT APPLICATION NUMBER: US/10/482,524  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB 0115570.4  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: GB 0205604.2  
; PRIOR FILING DATE: 2002-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-482-524-4

Query Match 97.3%; Score 2024; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 3e-164;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 MSGRPTTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQBSVYTDTK 70  
Db 1 MSGRPTTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQBSVYTDTK 60  
QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130  
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120  
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYQLFRSLAYIHSFGICHR 190  
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYQLFRSLAYIHSFGICHR 180  
QY 191 DIKPNLLDDPDTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
Db 181 DIKPNLLDDPDTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310  
Db 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300  
QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 370  
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360  
RESULT 8  
US-10-772-636-72  
; Sequence 72, Application US/10772636  
; Publication No. US20050042687A1  
; GENERAL INFORMATION:  
; APPLICANT: Kelly, Louise M.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Farlow, Deborah  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,  
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,  
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,  
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,  
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR  
; FILE REFERENCE: MPI03-015PIRNONMIM  
; CURRENT APPLICATION NUMBER: US/10/772,636  
; CURRENT FILING DATE: 2004-02-05  
; PRIOR APPLICATION NUMBER: US 60/445,241  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,389  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/456,320  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/460,279  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/465,924  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/470,052  
; PRIOR FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: US 60/498,106  
; PRIOR FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US 60/500,179  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US 60/502,909  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/510,351  
; PRIOR FILING DATE: 2003-10-10  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-772-636-72

Query Match 97.3%; Score 2024; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 3e-164;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 MSGRPTTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQBSVYTDTK 70  
Db 1 MSGRPTTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQBSVYTDTK 60  
QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130  
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120  
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYQLFRSLAYIHSFGICHR 190  
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYQLFRSLAYIHSFGICHR 180  
QY 191 DIKPNLLDDPDTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
Db 181 DIKPNLLDDPDTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310  
Db 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300  
QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 370  
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
Db 361 NFFTQELSSNPPLATILIPPHARI 384  
RESULT 9  
US-10-689-461-1

; Sequence 1, Application US/10689461  
; Publication No. US2005004851A1  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Ng, Doris G.  
; APPLICANT: Ng, Steve H.  
; APPLICANT: Medina-Selby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/10/689,461  
; CURRENT FILING DATE: 2003-10-20  
; PRIOR APPLICATION NUMBER: US/10/211,412  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US/09/916,109  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-689-461-1

Query Match 97.3%; Score 2024; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 3e-164;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 MSGRPRTTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVATPGQGPDRPQEVSYDTDK 70  
DB 1 MSGRPRTTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVATPGQGPDRPQEVSYDTDK 60  
  
QY 71 VINGSGFVVYQAKLDCSGLVAIKVLODKRPNRELQIMRKLDHCNIVRLRYFFYSYG 130  
DB 61 VINGSGFVVYQAKLDCSGLVAIKVLODKRPNRELQIMRKLDHCNIVRLRYFFYSYG 120  
  
QY 131 EKDEYVLNLVDYVETVYVARHYSRAKQTLPVLYVKLYQLFRSLAYIHSFGICHR 190  
DB 121 EKDEYVLNLVDYVETVYVARHYSRAKQTLPVLYVKLYQLFRSLAYIHSFGICHR 180  
  
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DB 181 DIKPQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYSIDV 240  
  
QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310  
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QY 311 WTKVFRPTPEAIACSLLEVTPTARLTPEACAHSPFDELDRDNNVHPNGRDTPALF 370  
DB 301 WTKVFRPTPEAIACSLLEVTPTARLTPEACAHSPFDELDRDNNVHPNGRDTPALF 360  
  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 10  
US-10-840-060-257  
; Sequence 257, Application US/10840060  
; Publication No. US20050227243A1  
; GENERAL INFORMATION:  
; APPLICANT: Cyclacel Limited  
; APPLICANT: Deak, Peter  
; APPLICANT: Frenz, Lisa  
; APPLICANT: Glover, David  
; APPLICANT: Midgley, Carol  
; TITLE OF INVENTION: Cell Cycle Progression Proteins  
; FILE REFERENCE: 10069/2012  
; CURRENT APPLICATION NUMBER: US/10/840,060

; CURRENT FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: PCT/GB02/04780  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: GB 0126506.5  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: GB 0128384.5  
; PRIOR FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: GB 0203185.4  
; PRIOR FILING DATE: 2002-02-11  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 257  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-840-060-257

Query Match 97.3%; Score 2024; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 3e-164;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 131 EKDEYVLNLVDYVETVYVARHYSRAKQTLPVLYVKLYQLFRSLAYIHSFGICHR 190  
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QY 191 DIKPQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYSIDV 250  
DB 181 DIKPQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYSIDV 240  
  
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DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300  
  
QY 311 WTKVFRPTPEAIACSLLEVTPTARLTPEACAHSPFDELDRDNNVHPNGRDTPALF 370  
DB 301 WTKVFRPTPEAIACSLLEVTPTARLTPEACAHSPFDELDRDNNVHPNGRDTPALF 360  
  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 11  
US-11-288-493-72  
; Sequence 72, Application US/11288493  
; Publication No. US20060078947A1  
; GENERAL INFORMATION:  
; APPLICANT: Kelly, Louise M.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Farlow, Deborah  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,  
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,  
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,  
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,  
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR  
; TITLE OF INVENTION: 5014  
; FILE REFERENCE: MPI03-015PIRNONMIN  
; CURRENT APPLICATION NUMBER: US/11/288,493  
; CURRENT FILING DATE: 2005-11-29  
; PRIOR APPLICATION NUMBER: US/10/772,636  
; PRIOR FILING DATE: 2004-02-05  
; PRIOR APPLICATION NUMBER: US 60/445,241  
; PRIOR FILING DATE: 2003-02-05

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; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-288-493-72

Query Match
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Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKDEVTNLVLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVTNLVLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDPDTAVLKCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
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DB 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 12
US-10-746-545-31
; Sequence 31, Application US/10746545
; Publication No. US2004011075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphra Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L.
; APPLICANT: Petillo, Peter A.
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Patent in version 3.2
; SEQ ID NO 31
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-746-545-31

Query Match
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Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKDEVTNLVLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVTNLVLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
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QY 311 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 13
US-10-278-759-6
; Sequence 6, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278,759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-278-759-6

Query Match
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QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 130
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QY 191 DIKPNLLDPDPTAVLKCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
DB 181 DIKPNLLDPDPTAVLKCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
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QY 311 WTKVFRPRTPEAIALCSRLLVPTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370  
DB 301 WTKVFRPRTPEAIALCSRLLVPTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360  
QY 371 NFTTQELSSNPPLATILIPPHARI 394  
DB 361 NFTTQELSSNPPLATILIPPHARI 384  
RESULT 14  
US-10-135-255-1  
; Sequence 1, Application US/10135255  
; Publication No. US2003012532A1  
; GENERAL INFORMATION:  
; APPLICANT: TER HAAR, ERNST  
; APPLICANT: SWENSON, LOVORKA  
; APPLICANT: GREEN, JEREMY  
; APPLICANT: ARNOST, MICHAEL J.  
; TITLE OF INVENTION: INHIBITORS OF GSK-3 AND CRYSTAL STRUCTURES OF GSK-3B  
; TITLE OF INVENTION: PROTEIN AND PROTEIN COMPLEXES  
; FILE REFERENCE: VPI/01-02  
; CURRENT APPLICATION NUMBER: US/10/135,255  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: 60/361,899  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: 60/297,094  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: 60/287,366  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-135-255-1

Query Match 96.7%; Score 2013; DB 4; Length 420;  
Best Local Similarity 99.7%; Pred. No. 2.6e-163;  
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDKRRFNRELQIMRKLHDHCNIVRLRYFFYS 130  
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QY 131 EKDEVYLVNLDYVPETVYRVARHYSRAKQTLFVIYVKLYMYQLFRSLAYIHSFGICHR 190  
DB 121 EKDEVYLVNLDYVPETVYRVARHYSRAKQTLFVIYVKLYMYQLFRSLAYIHSFGICHR 180  
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DB 181 DIKPNLLDPDPTAVLKCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
QY 251 WSAGCVLAELLGQIPFGDGVQDLVEIHKVLTGTPREQIREMNPNTYEFKFPQIKAH 310  
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QY 311 WTKVFRPRTPEAIALCSRLLVPTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370  
DB 301 WTKVFRPRTPEAIALCSRLLVPTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360  
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DB 361 NFTTQELSSNPPLATILIPPHARI 384

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Job time : 185 secs

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RESULT 15  
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; Sequence 15, Application US/10746545  
; Publication No. US20040171075A1  
; GENERAL INFORMATION:  
; APPLICANT: Deciphra Pharmaceuticals, Inc.  
; APPLICANT: Flynn, Daniel L  
; APPLICANT: Petillo, Peter A  
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES  
; FILE REFERENCE: 34475  
; CURRENT APPLICATION NUMBER: US/10/746,545  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/437,487  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-746-545-15  
Query Match 96.7%; Score 2013; DB 4; Length 420;  
Best Local Similarity 99.7%; Pred. No. 2.6e-163;  
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 MSGRPRRTTSAESCCKPVQPSAFSGSMKVSVDKDGSKVTTVATPGQGPDRPQEVSYDTDK 70  
DB 1 MSGRPRRTTSAESCCKPVQPSAFSGSMKVSVDKDGSKVTTVATPGQGPDRPQEVSYDTDK 60  
QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDKRRFNRELQIMRKLHDHCNIVRLRYFFYS 130  
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QY 371 NFTTQELSSNPPLATILIPPHARI 394  
DB 361 NFTTQELSSNPPLATILIPPHARI 384

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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:12:25 ; Search time 51 Seconds  
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676.217 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
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- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2081	100.0	394	2	US-09-916-109-2
2	2081	100.0	394	2	US-10-211-412B-2
3	2024	97.3	420	2	US-09-336-038-1
4	2024	97.3	420	2	US-09-916-109-1
5	2024	97.3	420	2	US-10-211-412B-1
6	2024	97.3	420	2	US-09-538-092-1163
7	2010	96.6	420	1	US-08-602-264A-14
8	1883.5	90.5	361	2	US-09-916-109-3
9	1883.5	90.5	361	2	US-10-211-412B-3
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11	1609	77.3	447	2	US-10-211-412B-5
12	1609	77.3	483	2	US-09-916-109-4
13	1609	77.3	483	2	US-10-211-412B-4
14	1609	77.3	483	2	US-09-538-092-1162
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16	1588	76.3	351	2	US-10-211-412B-7
17	1588	76.3	387	2	US-09-916-109-6
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21	1242	59.7	410	2	US-09-347-801-10
22	1242	59.7	410	2	US-09-854-731-10
23	1240	59.6	402	2	US-09-347-801-16
24	1240	59.6	402	2	US-09-854-731-16
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26	1232	59.2	405	2	US-09-854-731-20

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28	1232	59.2	407	2	US-09-854-731-23	Sequence 23, Appl
29	1226	58.9	411	2	US-09-347-801-22	Sequence 22, Appl
30	1226	58.9	411	2	US-09-854-731-22	Sequence 22, Appl
31	1165.5	56.0	399	2	US-09-347-801-14	Sequence 14, Appl
32	1165.5	56.0	399	2	US-09-854-731-14	Sequence 14, Appl
33	1001.5	48.1	395	2	US-09-248-796A-18499	Sequence 18499, A
34	940	45.2	370	2	US-09-538-092-623	Sequence 623, App
35	674	32.4	411	2	US-09-248-796A-18500	Sequence 18500, A
36	521.5	25.1	146	2	US-09-270-767-43078	Sequence 43078, A
37	483.5	23.2	649	2	US-09-949-016-10147	Sequence 10147, A
38	478.5	23.0	334	2	US-09-949-016-10777	Sequence 10777, A
39	476.5	22.9	379	2	US-09-411-628-14	Sequence 14, Appl
40	476.5	22.9	379	2	US-10-174-794-14	Sequence 14, Appl
41	476.5	22.9	379	2	US-09-538-092-1021	Sequence 1021, Ap
42	472.5	22.7	379	2	US-08-622-277A-8	Sequence 8, Appl
43	472.5	22.7	379	2	US-09-025-580-25	Sequence 25, Appl
44	472.5	22.7	379	2	US-09-642-749-25	Sequence 25, Appl
45	472.5	22.7	631	2	US-09-417-197-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1  
US-09-916-109-2  
; Sequence 2, Application US/09916109  
; Patent No. 6465231  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Colt, Doris G.  
; APPLICANT: Nguyen, Steve H.  
; APPLICANT: Medina-Selby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/09/916,109  
; CURRENT FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-916-109-2

Query Match	100.0%;	Score 2081;	DB 2;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 3.1e-221;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEYPMEEGGMSGRPRRTTSFAESCKPQOPSAGFSKMSVRDCKGSKVTTVVATPGQCPDR	60	
Db	1	MEYPMEEGGMSGRPRRTTSFAESCKPQOPSAGFSKMSVRDCKGSKVTTVVATPGQCPDR	60	
Qy	61	PQEVSYTDTKVIENGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV	120	
Db	61	PQEVSYTDTKVIENGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIV	120	
Qy	121	RLRYFFYSSEKKDEVVLNVLVDYVPTVTVARHYSRAKQTLPVIVVKLYMYQLFRSLA	180	
Db	121	RLRYFFYSSEKKDEVVLNVLVDYVPTVTVARHYSRAKQTLPVIVVKLYMYQLFRSLA	180	
Qy	181	YIHSFGICHRDIPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSVRYRAPELIFG	240	
Db	181	YIHSFGICHRDIPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSVRYRAPELIFG	240	
Qy	241	ATDYTSSIDVMSAGCVLAELLGQIPPGDSQGVQDLVEIIVKVLGTPTRREQIRENNPNYTE	300	
Db	241	ATDYTSSIDVMSAGCVLAELLGQIPPGDSQGVQDLVEIIVKVLGTPTRREQIRENNPNYTE	300	



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Qy 301 FKFPQIKAHPTKVFRTPTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 360
Db 301 FKFPQIKAHPTKVFRTPTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 360

Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 2
US-10-211-412B-2
; Sequence 2, Application US/10211412B
; Patent No. 671624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211.412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916.109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-2

Query Match 100.0%; Score 2081; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-221;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEYMPMEGGNSGRPTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDR 60
Db 1 MEYMPMEGGNSGRPTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDR 60

Qy 61 POEVSYTDTKVINGSGFGVYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120
Db 61 POEVSYTDTKVINGSGFGVYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIV 120

Qy 121 RLRYFFYSSEKDEVLNLVDYVPETVYVARHYSRAKOTLPVIYVKLYMYQLFRSLA 180
Db 121 RLRYFFYSSEKDEVLNLVDYVPETVYVARHYSRAKOTLPVIYVKLYMYQLFRSLA 180

Qy 181 YHSFGICHRIKPNQLLLDPTAVLKCDPFGSAKQLVGRPNVSYICSYRYRAPELIFG 240
Db 181 YHSFGICHRIKPNQLLLDPTAVLKCDPFGSAKQLVGRPNVSYICSYRYRAPELIFG 240

Qy 241 ATDTSSIDVNSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTREIREMNPNTY 300
Db 241 ATDTSSIDVNSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTREIREMNPNTY 300

Qy 301 KFQPOIKAHPTKVFRTPTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 360
Db 301 KFQPOIKAHPTKVFRTPTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 360

Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 3
US-09-336-038-1
; Sequence 1, Application US/09336038
; Patent No. 6417185
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; GENERAL INFORMATION:
; APPLICANT: Goff, Dane
; APPLICANT: Harrison, Steven
; APPLICANT: Nuss, John
; APPLICANT: Ring, David B.
; APPLICANT: Zhou, Xiaohui A.
; TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
; FILE REFERENCE: 1443.003
; CURRENT APPLICATION NUMBER: US/09/336.038
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/089,978
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-038-1

Query Match 97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.9e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYDTK 70
Db 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYDTK 60

Qy 71 VINGSGFGVYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 130
Db 61 VINGSGFGVYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120

Qy 131 EKDEVYLNLDYVPETVYVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDYVPETVYVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNQLLLDPTAVLKCDPFGSAKQLVGRPNVSYICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNQLLLDPTAVLKCDPFGSAKQLVGRPNVSYICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTREIREMNPNTYFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTREIREMNPNTYFKFPQIKAH 300

Qy 311 WTKVFRPRTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPAL 370
Db 301 WTKVFRPRTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPAL 360

Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4
US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916.109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-1

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 120

Qy 131 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGDSGVQDLVEI IKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLGGPIPPGDSGVQDLVEI IKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEALCALCSRLLEYTP TARLTPLEACAHSFDFELRDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCALCSRLLEYTP TARLTPLEACAHSFDFELRDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412B-1
; Sequence 1, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211.412B
; PRIOR FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-1

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 120

Qy 131 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGDSGVQDLVEI IKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLGGPIPPGDSGVQDLVEI IKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEALCALCSRLLEYTP TARLTPLEACAHSFDFELRDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCALCSRLLEYTP TARLTPLEACAHSFDFELRDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 6
US-09-538-092-1163
; Sequence 1163, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1163
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49841
US-09-538-092-1163

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNI VRLRYFFYSYG 120

Qy 131 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVYPETVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNQLLLDPDTAVLKLCDGSAKQLVRGEPNVS YICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGDSGVQDLVEI IKVLGTPTREQIREMNPNTYEFKFPQIKAH 310

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Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTTTREQIREMNPNTYTFEPQIKAHF 300  
QY 311 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVKHPNGRDTPALF 370  
Db 301 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVKHPNGRDTPALF 360  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
Db 361 NFFTQELSSNPPLATILIPPHARI 384  
RESULT 7  
US-08-602-264A-14  
; Sequence 14, Application US/08602264A  
; Patent No. 5837853  
; GENERAL INFORMATION:  
; APPLICANT: AKIHICO TAKASHIMA et al.  
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR  
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE  
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: WENDEROTH, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 144 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,264A  
; FILING DATE: February 20, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/204,091  
; FILING DATE: March 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 420 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM: human being  
US-08-602-264A-14  
Query Match 96.6%; Score 2010; DB 1; Length 420;  
Best Local Similarity 99.5%; Pred. No. 2.56-213;  
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 11 MSORPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDPQSVSYDTDK 70  
Db 1 MSORPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDPQSVSYDTDK 60  
QY 71 VIGNSGFVVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKL DHCNIVRLRYFFSSG 130  
Db 61 LIGNSGFVVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKL DHCNIVRLRYFFSSG 120  
QY 131 EKKDEVYLNLDVVPETVYVARHYSRKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 190

Db 121 EKKDEVYLNLDVVPETVYVARHYSRKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 180  
QY 191 DIKPQNLLDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIPGATDYTSSIDV 250  
Db 181 DIKPQNLLDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIPGATDYTSSIDV 240  
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTTTREQIREMNPNTYTFEPQIKAHF 310  
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTTTREQIREMNPNTYTFEPQIKAHF 300  
QY 311 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVKHPNGRDTPALF 370  
Db 301 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVKHPNGRDTPALF 360  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
Db 361 NFFTQELSSNPPLATILIPPHARI 384  
RESULT 8  
US-09-916-109-3  
; Sequence 3, Application US/09916109  
; Patent No. 6465231  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Coit, Doris G.  
; APPLICANT: Nguyen, Steve H.  
; APPLICANT: Medina-Selby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/09/916,109  
; CURRENT FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-916-109-3  
Query Match 90.5%; Score 1883.5; DB 2; Length 361;  
Best Local Similarity 91.6%; Pred. No. 1.9e-199;  
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
QY 1 MEYMPMEGGGMSGRPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDP 60  
Db 1 MEYMPMEGGG-----GSKVTTVVATPGQGPDP 27  
QY 61 PORVSYTDTKVIGNGSFGVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKL DHCNIV 120  
Db 28 PORVSYTDTKVIGNGSFGVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKL DHCNIV 87  
QY 121 RLRYFFYSSEKKEDEVYLNLDVVPETVYVARHYSRKQTLPIVYVVKLYMYQLFRSLA 180  
Db 88 RLRYFFYSSEKKEDEVYLNLDVVPETVYVARHYSRKQTLPIVYVVKLYMYQLFRSLA 147  
QY 181 YIHSFGICHRDIKPQNLLDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFG 240  
Db 148 YIHSFGICHRDIKPQNLLDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFG 207  
QY 241 ATDYTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTTTREQIREMNPNTY 300  
Db 208 ATDYTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTTTREQIREMNPNTY 267  
QY 301 FKPPQIKAHFWTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVK 360  
Db 268 FKPPQIKAHFWTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSEFFDELDPNVK 327

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QY 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 361

RESULT 9
US-10-211-412B-3
; Sequence 3, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-211-412B-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.9e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 MEYMPMEGGMSGRPTTSFABSCKPVQPSAFGSMKVRSDKSGKVTTVATPGQGPDR 60
Db 1 MEYMPMEGGG-----GSKVTTVATPGQGPDR 27

QY 61 POEVSYTDTKVINGSGFVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIV 120
Db 28 POEVSYTDTKVINGSGFVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIV 87

QY 121 RLRYFFYSSEKKEDEVYLVLDVYPETVYVARHYSRAKQTLPLVIYVKLYMYQLFRSLA 180
Db 88 RLRYFFYSSEKKEDEVYLVLDVYPETVYVARHYSRAKQTLPLVIYVKLYMYQLFRSLA 147

QY 181 YIHSFGICHRDIKPNLLDPPDTAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFG 240
Db 148 YIHSFGICHRDIKPNLLDPPDTAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFG 207

QY 241 ADYTSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIREMNNPYTE 300
Db 208 ADYTSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIREMNNPYTE 267

QY 301 FKPPQIKAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKH 360
Db 268 FKPPQIKAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKH 327

QY 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 361

RESULT 10
US-09-916-109-5
; Sequence 5, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
```

```
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-916-109-5

Query Match 77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.7e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFABSCKPVQPSAFGSMKVRSDKSGKVTTVATPGQGPDRPOEVS 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLGK--DSGKVTTVATLGGQSPERSQEVAY 119

QY 67 TDTKVIINGSGFVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIVRLRYFF 126
Db 120 TDTKVIINGSGFVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIVRLRYFF 179

QY 127 YSSGEKKDEVYLVLDVYPETVYVARHYSRAKQTLPLVIYVKLYMYQLFRSLAYTHSFG 186
Db 180 YSSGEKKDEVYLVLDVYPETVYVARHYSRAKQTLPLVIYVKLYMYQLFRSLAYTHSFG 239

QY 187 ICHRDIKPNLLDPPDTAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPNLLDPPDTAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 299

QY 247 SIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIREMNNPYTEFKPQI 306
Db 300 SIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIREMNNPYTEFKPQI 359

QY 307 KAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKHGRDT 366
Db 360 KAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKHGRDT 419

QY 367 PALFNFSTOELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAILIPPHLR 446

RESULT 11
US-10-211-412B-5
; Sequence 5, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447
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! TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-5

Query Match 77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.7e-169; Indels 14; Gaps 3;
Matches 312; Conservative 24; Mismatches 37;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDQSGSKVTTVATPGGPRPQEVSY 66
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QY 67 TDTKVINGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKNRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDIKVIINGSGFVVYQARLAETRELVAIKKVLQDKFKFKNRELQIMRKLDHCNIVRLRYFF 179

QY 127 YSSGEKKDEVILNLVDYVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLAYTHSPG 186
Db 180 YSSGEKKDELYLNLVLEYVETVYRVARHFTTAKLTIPILYKVMYQLFRSLAYTHSQG 239

QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 299

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Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQVLEIKVLTPTREQIREMNPNTYEFKPPQI 359

QY 307 KAHPTWKVFRPRTTPEAIALCSRLLEYTPTARLTPLCAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWKVFKSRTTPEAIALCSLLLEYTPTSSRLSPLECAHSPFDELCLGTQLPNNRPL 419

QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAIILIPHLR 446

RESULT 12
US-09-916-109-4
; Sequence 4, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-4

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Matches 312; Conservative 24; Mismatches 37;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDQSGSKVTTVATPGGPRPQEVSY 66
Db 73 GCGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119

QY 67 TDTKVINGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKNRELQIMRKLDHCNIVRLRYFF 126
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QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 299

QY 247 SIDWSAGCVLAELLGQPIFFGDSGVDQVLEIKVLTPTREQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQVLEIKVLTPTREQIREMNPNTYEFKPPQI 359

QY 307 KAHPTWKVFRPRTTPEAIALCSRLLEYTPTARLTPLCAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWKVFKSRTTPEAIALCSLLLEYTPTSSRLSPLECAHSPFDELCLGTQLPNNRPL 419

QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAIILIPHLR 446

RESULT 12
US-10-211-412B-4
; Sequence 4, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-4

Query Match 77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 7.6e-169; Indels 14; Gaps 3;
Matches 312; Conservative 24; Mismatches 37;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDQSGSKVTTVATPGGPRPQEVSY 66
Db 73 GCGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119

QY 67 TDTKVINGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKNRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDIKVIINGSGFVVYQARLAETRELVAIKKVLQDKFKFKNRELQIMRKLDHCNIVRLRYFF 179

QY 127 YSSGEKKDEVILNLVDYVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLAYTHSPG 186
Db 180 YSSGEKKDELYLNLVLEYVETVYRVARHFTTAKLTIPILYKVMYQLFRSLAYTHSQG 239

QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYS 299

QY 247 SIDWSAGCVLAELLGQPIFFGDSGVDQVLEIKVLTPTREQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQVLEIKVLTPTREQIREMNPNTYEFKPPQI 359
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QY 307 KAHPTWKVFRPRTPEAIALCSRLLEYTPVARTPLLEACAHSPFDELDPNVKHPNGRDT 366  
Db 360 KAHPTWKVFRPRTPEAIALCSRLLEYTPSSRLSPLEACAHSPFDELRCGLGTQLPNNRPL 419  
QY 367 PALPNTTQELSSNPPLATILIPPHAR 393  
Db 420 PPLNFNSAGELSIOQSLNAILIPPHLR 446

RESULT 14

US-09-538-092-1162  
; Sequence 1162, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqFormatter Version 0.9  
; SEQ ID NO 1162  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number P49840  
US-09-538-092-1162

Query Match 77.3%; Score 1609; DB 2; Length 483;  
Best Local Similarity 80.6%; Pred. No. 7.6e-169;  
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GCGMSGRPRT-TSFAESCKVQPSAFSGSKVSRDQKSGKVTWVATPGQDPDPQEVSY 66  
Db 73 GGGSGGPGAGTSFPPP-----GVKLR--DSGKVTTWATLGGQSPERSQEVAY 119  
QY 67 TDFKTVGNISFGVYQAKLDSGELVAIKVLDQKFKRELQIMRKLCHNCNIVRLRYFF 126  
Db 120 TDIKTVGNISFGVYQARLAETRELVAIKVLDQKFKRELQIMRKLCHNCNIVRLRYFF 179  
QY 127 YSSGEKKDEYVNLVLDYVPETVYRVARHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSFG 186  
Db 180 YSSGEKKDEYVNLVLDYVPETVYRVARHFTKAKLTIPILYVYKLYMYQLFRSLAYIHSQ 239  
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Db 240 VCHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSVYICSRYYRAPELIFGATDYS 299  
QY 247 SIDVWSAGCVLAELLLGQIFPGDSGVDQVLEIKVLGTPTREQIREMNPNTYEFKFPQI 306  
Db 300 SIDVWSAGCVLAELLLGQIFPGDSGVDQVLEIKVLGTPTREQIREMNPNTYEFKFPQI 359  
QY 307 KAHPTWKVFRPRTPEAIALCSRLLEYTPVARTPLLEACAHSPFDELDPNVKHPNGRDT 366  
Db 360 KAHPTWKVFRPRTPEAIALCSRLLEYTPSSRLSPLEACAHSPFDELRCGLGTQLPNNRPL 419  
QY 367 PALPNTTQELSSNPPLATILIPPHAR 393  
Db 420 PPLNFNSAGELSIOQSLNAILIPPHLR 446

RESULT 15

US-09-916-109-7  
; Sequence 7, Application US/09916109  
; Patent No. 6465231

; GENERAL INFORMATION:  
; APPLICANT: Harrison, Stephen D.  
; APPLICANT: Hall, John A.  
; APPLICANT: Calderon-Cacia, Maria  
; APPLICANT: Zhong, Ziyang  
; APPLICANT: Fang, Eric Y.  
; APPLICANT: Coit, Doris G.  
; APPLICANT: Nguyen, Steve H.  
; APPLICANT: Medina-Selby, Angelica  
; TITLE OF INVENTION: GSK3 POLYPEPTIDES  
; FILE REFERENCE: PP-15876.002/200130.524  
; CURRENT APPLICATION NUMBER: US/09/916,109  
; CURRENT FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-916-109-7

Query Match 76.3%; Score 1588; DB 2; Length 351;  
Best Local Similarity 86.2%; Pred. No. 9.5e-167;  
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 46 KVTTVATPGQDPDPQEVSYTDKTVIGNSFGVYQAKLDSGELVAIKVLDQKFKN 105  
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QY 106 RELQIMRKLCHNCNIVRLRYFFYSSEKKDEYVNLVLDYVPETVYRVARHYSRAKQTLPV 165  
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QY 166 IYVKLYMYQLFRSLAYIHSQGVCHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSV 225  
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QY 226 YICSRYYRAPELIFGATDYSIDVWSAGCVLAELLLGQIFPGDSGVDQVLEIKVLGT 285  
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QY 286 PTREQIREMNPNTYEFKFPQIKAHPTWKVFRPRTPEAIALCSRLLEYTPVARTPLLEAC 345  
Db 243 PTREQIREMNPNTYEFKFPQIKAHPTWKVFRPRTPEAIALCSRLLEYTPSSRLSPLEAC 302  
QY 346 AHSFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 393  
Db 303 AHSFFDELRCGLGTQLPNNRPLPPLNFNSAGELSIOQSLNAILIPPHLR 350

Search completed: September 15, 2006, 17:13:51  
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:04:00 ; Search time 302 Seconds  
(without alignments)  
1206.808 Million cell updates/sec

Title: US-10-733-816-2  
Perfect score: 2081  
Sequence: 1 MEYMPMEGMSGRPTTSP.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	96.7	420	1	GSK3B_HUMAN
2	2013	96.7	420	1	GSK3B_MOUSE
3	2013	96.7	420	2	G6F127_HUMAN
4	2013	96.7	420	2	Q5KU03_MOUSE
5	2010	96.6	420	1	GSK3B_RAT
6	2006	96.4	420	2	Q5YJC2_SPECI
7	1959	94.1	421	2	Q9IBD2_BRARE
8	1959	94.1	421	2	Q9YH60_BRARE
9	1931	92.8	420	2	Q91757_XENLA
10	1923	92.4	420	2	Q91627_XENLA
11	1793.5	86.2	496	2	Q4S0H0_TETNG
12	1704.5	81.9	440	2	Q9YH61_BRARE
13	1669.5	80.2	435	2	Q9IBD3_BRACHYDANIO
14	1666.5	80.1	407	2	Q9N143_CIONA
15	1632	78.4	414	2	Q61UG5_LYTWA
16	1614	77.6	414	2	Q46150_PARLI
17	1609	77.3	483	1	GSK3A_HUMAN
18	1607	77.2	483	1	GSK3A_RAT
19	1606	77.2	399	2	Q4SSG6_TETNG
20	1594	76.6	388	2	Q68D16_HUMAN
21	1565	75.2	363	2	Q7QA46_ANOGA
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23	1495.5	71.9	443	2	Q4H118_SUBDO
24	1485	71.4	442	2	Q9GTK0_HYDAT
25	1443	69.3	431	2	Q58952_DUGJA
26	1343.5	64.6	362	2	Q9Y0C2_CAEBL
27	1342.5	64.5	362	2	Q9U2Q9_CAEBL
28	1341.5	64.5	359	2	Q5WNK0_CAEBR
29	1305.5	62.7	501	1	GSK3H_DROME
30	1302	62.6	402	2	Q4PH53_USTWA
31	1296	62.3	409	2	Q40886_PETHY

32	1294	62.2	423	2	Q6VM07_PHYPA	Q6vm07 physcomitre
33	1289.5	62.0	398	2	Q55X64_CRYNE	Q55x64 cryptococcu
34	1289.5	62.0	398	2	Q5KMR8_CRYNE	Q5kmr8 cryptococcu
35	1283	61.7	410	1	KSG5_ARATH	Q8vzd5 arabidopsis
36	1275.5	61.3	471	2	Q24139_TOBAC	Q24139 nicotiana t
37	1273.5	61.2	424	2	Q6VM11_PHYPA	Q6vm11 physcomitre
38	1273.5	61.2	471	2	O82029_TOBAC	O82029 nicotiana t
39	1273	61.2	401	2	Q6EUS4_ORYSA	Q6eus4 oryza sativ
40	1271	61.1	423	2	Q6VM08_PHYPA	Q6vm08 physcomitre
41	1269	61.0	412	2	Q4WDL1_ASPPU	Q4wdl1 aspergillus
42	1264	60.7	394	2	Q5AYX2_EMENI	Q5ayx2 aspergillus
43	1263.5	60.7	424	2	Q6AVQ3_ORYSA	Q6avq3 oryza sativ
44	1262.5	60.7	470	2	O82038_PETHV	O82038 petunia hyb
45	1262	60.6	355	2	Q6VM10_PHYPA	Q6vm10 physcomitre

## ALIGNMENTS

## RESULT 1

ID	GSK3B_HUMAN	STANDARD;	PRT;	420 AA.
AC	P49841; Q9BWH3; Q9UL47;			
DT	01-OCT-1996, integrated into UniProtKB/Swiss-Prot.			
DT	02-MAY-2002, sequence version 2.			
DT	07-MAR-2006, entry version 70.			
DE	Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).			
GN	Names=GSK3B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RX	MEDLINE=95071278; PubMed=7980435;			
RA	Stambolic V., Woodgett J.R.;			
RT	"Mitogen inactivation of glycogen synthase kinase-3 beta in intact			
RT	cells via serine 9 phosphorylation.";			
RL	Biochem. J. 303:701-704(1994).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).			
RC	TISSUE=Eye, and Placenta;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesey R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE OF 185-202.			
RX	MEDLINE=99455114; PubMed=10523816; DOI=10.1038/sj.mp.4000538;			
RA	Rhoads A.R., Karkera J.D., Detera-Wadleigh S.D.;			
RT	"Radiation hybrid mapping of genes in the lithium-sensitive wnt			
RT	signaling pathway.";			
RL	Mol. Psychiatry 4:437-442(1999).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE OF 1-28.			

RX MEDLINE=99417672; PubMed=10486203; DOI=10.1006/geno.1999.5875;  
 RA Lau K.F., Miller C.C.J., Anderton B.H., Shaw P.C.;  
 RT "Molecular cloning and characterization of the human glycogen synthase  
 RL kinase-3beta promoter.";   
 RN Genomics 60:121-128(1999).  
 RP [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;  
 RA Delcomenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;  
 RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen  
 RL synthase kinase 3 and protein kinase B/AKT by the integrin-linked  
 RP kinase.";   
 RN Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998).  
 RP [6]  
 RP INTERACTION WITH NIN.  
 RX MEDLINE=20461863; PubMed=11004522; DOI=10.1016/S0167-4781(00)00127-5;  
 RA Hong Y.-R., Chen C.-H., Chang J.-H., Wang S.-K., Sy W.-D., Chou C.-K.,  
 RL Hwang S.-L.;  
 RT "Cloning and characterization of a novel human ninein protein that  
 RL interacts with the glycogen synthase kinase 3beta.";   
 RN Biochim. Biophys. Acta 1492:513-516(2000).  
 RP [7]  
 RP PHOSPHORYLATION SITE THR-390.  
 RX PubMed=15302935; DOI=10.1073/pnas.0404720101;  
 RA Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,  
 RL Li J., Cohn M.A., Cantley L.C., Gygi S.P.;  
 RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";   
 RN Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).  
 RP [8]  
 RP CHARACTERIZATION WITH GSK3B.  
 RX PubMed=15752768; DOI=10.1016/j.bbrc.2005.02.089;  
 RA Hsu H.-C., Lee Y.-L., Cheng T.-S., Hwang S.-L., Chang L.-K., Lu P.-J.,  
 RL Hong Y.-R.;  
 RT "Characterization of two non-testis-specific CABYR variants that bind  
 RL to GSK3beta with a proline-rich extensin-like domain.";   
 RN Biochem. Biophys. Res. Commun. 329:1108-1117(2005).  
 RP [9]  
 RP PHOSPHORYLATION SITE TYR-216, AND MASS SPECTROMETRY.  
 RX PubMed=15592455; DOI=10.1038/nbt1046;  
 RA Rush J., Moxitt A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RL Zha X.-M., Polakiewicz R.D., Comb M.J.;  
 RT "Immunofluorescence profiling of tyrosine phosphorylation in cancer  
 RL cells.";   
 RN Nat. Biotechnol. 23:94-101(2005).  
 RP [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 35-386.  
 RX MEDLINE=21334149; PubMed=11440715; DOI=10.1016/S0092-8674(01)00374-9;  
 RA DeJani R., Fraser E., Roe S.M., Young N., Good V., Dale T.C.,  
 RL Pearl L.H.;  
 RT "Crystal structure of glycogen synthase kinase 3 beta: structural  
 RL basis for phosphate-primed substrate specificity and autoinhibition.";   
 RN Cell 105:721-732(2001).  
 RP [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 27-393 OF PHOSPHORYLATED  
 RP GSK3B.  
 RX MEDLINE=21605727; PubMed=11738041; DOI=10.1016/S0969-2126(01)00679-7;  
 RA Bax B., Carter P.S., Lewis C., Guy A.R., Bridges A., Tanner R.,  
 RL Pettman G., Mannix C., Culbert A.A., Brown M.J.B., Smith D.G.,  
 RA Reith A.D.;  
 RT "The structure of phosphorylated GSK-3beta complexed with a peptide,  
 RL FRATtide, that inhibits beta-catenin phosphorylation.";   
 RN Structure 9:1143-1152(2001).  
 RP [12]  
 RP FUNCTION: Participates in the Wnt signaling pathway. Implicated in  
 CC the hormonal control of several regulatory proteins including  
 CC glycogen synthase, MYB and the transcription factor JUN.  
 CC Phosphorylates JUN at sites proximal to its DNA-binding domain,  
 CC thereby reducing its affinity for DNA.  
 CC [13]  
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC [14]  
 CC ENZYME REGULATION: Inhibited when phosphorylated by AKT1.  
 CC [15]  
 CC SUBUNIT: Monomer (By similarity). Interacts with NIN and CABYR.  
 CC [16]  
 CC INTERACTION:  
 CC Q72693:UPF3A; NbExp=1; IntAct=EBI-373586; EBI-372587;  
 CC [17]  
 CC ALTERNATIVE PRODUCTS:  
 CC

CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P49841-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P49841-2; Sequence=VSP\_004790;  
 CC Note=No experimental confirmation available;  
 CC [18]  
 CC TISSUE SPECIFICITY: Expressed in testis, thymus, prostate and  
 CC ovary and weakly expressed in lung, brain and kidney.  
 CC [19]  
 CC PTM: Phosphorylated by AKT1 and ILK1.  
 CC [20]  
 CC SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3  
 CC subfamily.  
 CC [21]  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC [22]  
 CC ENBL; L33801; AAA66475.1; -; mRNA.  
 CC ENBL; BC000251; AAH00251.1; -; mRNA.  
 CC ENBL; BC012760; AAH12760.1; -; mRNA.  
 CC ENBL; AF098789; AAC69340.1; -; Genomic\_DNA.  
 CC ENBL; AF074333; AAD48517.1; -; Genomic\_DNA.  
 CC PIR; S53324; S53324.  
 CC PDB; 1GNG; X-ray; A/B=27-393.  
 CC PDB; 1H8F; X-ray; A/B=35-386.  
 CC PDB; 1I09; X-ray; A/B=1-420.  
 CC PDB; 1J1B; X-ray; A/B=1-420.  
 CC PDB; 1J1C; X-ray; A/B=1-420.  
 CC PDB; 1O9U; X-ray; A/B=1-420.  
 CC PDB; 1PYX; X-ray; A/B=1-420.  
 CC PDB; 1Q3D; X-ray; A/B=2-420.  
 CC PDB; 1Q3W; X-ray; A/B=2-420.  
 CC PDB; 1Q41; X-ray; A/B=2-420.  
 CC PDB; 1Q4L; X-ray; A/B=2-420.  
 CC PDB; 1Q5K; X-ray; A/B=7-420.  
 CC PDB; 1R0E; X-ray; A/B=35-420.  
 CC PDB; 1UV5; X-ray; A/B=35-384.  
 CC IntAct; P49841; -; Homo sapiens.  
 CC Ensembl; ENSG00000082701; Homo sapiens.  
 CC H-InvDB; HIX0003589; -;  
 CC HGNC; HGNC:4617; GSK3B.  
 CC MIM; 605004; Gene.  
 CC LinkHub; P49841; -;  
 CC GO; GO:0004696; F:glycogen synthase kinase 3 activity; TAS.  
 CC GO; GO:0005515; P:protein binding; IPI.  
 CC GO; GO:0005777; P:glycogen metabolism; TAS.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.  
 CC InterPro; IPR001245; Tyr\_kinase.  
 CC Pfam; PF00069; Kinase; 1.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00220; S\_TKc; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 CC 3D-structure; Alternative splicing; ATP-binding; Kinase;  
 CC Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;  
 CC Transferase; Wnt signaling pathway.  
 CC CHAIN 1 420 Glycogen synthase kinase-3 beta.  
 CC /FTID=PRO\_0000085980.  
 CC DOMAIN 56 340 Protein kinase.  
 CC NP\_BIND 62 70 ATP (By similarity).  
 CC ACT\_SITE 181 181 Proton acceptor.  
 CC BIND 85 85 ATP (By similarity).  
 CC MOD\_RES 9 9 Phosphoserine (by PKB/AKT1).  
 CC MOD\_RES 216 216 Phosphotyrosine.  
 CC MOD\_RES 389 389 Phosphoserine (By similarity).  
 CC MOD\_RES 390 390 Phosphothreonine.  
 CC VARSPPLIC 303 303 K->KDSGCTGFTSGVR (in isoform 2).  
 CC /FTID=VSP\_004790.  
 CC MUTAGEN 9 9 S->A: Loss of phosphorylation;  
 CC insensitive to inhibitory  
 CC phosphorylation.  
 CC V->G (in Ref. 4).  
 CC CONFLICT 28 28

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FT  CONFLICT  350  350  L -> H (in Ref. 1).
FT  STRAND    38  48
Query Match  96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11  MSGRPRTTSFAESCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db  1  MSGRPRTTSFAESCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60

Qy  71  VINGSGVVYQAKLDCSGELVAIKVLDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
Db  61  VINGSGVVYQAKLDCSGELVAIKVLDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120

Qy  131  EKDEVVNLVLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYOLFSLAYIHSFGICHR 190
Db  121  EKDEVVNLVLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYOLFSLAYIHSFGICHR 180

Qy  191  DIKPNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
Db  181  DIKPNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240

Qy  251  WSAGCVLAELLGQPIPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 310
Db  241  WSAGCVLAELLGQPIPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 300

Qy  311  WTKVFRPTPEALACSLRLLEYPPTARLTPLCAHSAFDELDPNVKHPNGRDTPALF 370
Db  301  WTKVFRPTPEALACSLRLLEYPPTARLTPLCAHSAFDELDPNVKHPNGRDTPALF 360

Qy  371  NFFTQELSSNPPLATILIPPHARI 394
Db  361  NFFTQELSSNPPLATILIPPHARI 384

RESULT 2
GSK3B_MOUSE
ID  GSK3B_MOUSE  STANDARD;  PRT;  420 AA.
AC  Q9WV60;
DC  01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT  01-MAY-2000, sequence version 2.
DE  Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).
GN  Name=Gsk3b;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [MRNA].
RC  Tissue=Testis;
RA  Salameh W.A., Guo T.B., Chan K.C., Mitchell A.P.;
RT  "Testicular expression and hormonal control of glycogen synthase
RL  kinase 3, a homologue of yeast RIM1.",
RN  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC  STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

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RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.",
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [3]
RP  PHOSPHORYLATION SITE SER-389, AND MASS SPECTROMETRY.
RX  PubMed=15345747; DOI=10.1074/mcp.M400085-MCP200;
RA  Ballif B.A., Villen J., Beausoleil S.A., Schwartz D., Gygi S.P.;
RT  "Phosphoproteomic analysis of the developing mouse brain.",
RL  Mol. Cell. Proteomics 3:1093-1101(2004).
RN  [4]
RP  PHOSPHORYLATION SITE TYR-216, AND MASS SPECTROMETRY.
RX  PubMed=15592455; DOI=10.1038/nbt1046;
RA  Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA  Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT  "Immunofluorescence profiling of tyrosine phosphorylation in cancer
RT  cells.",
RL  Nat. Biotechnol. 23:94-101(2005).
CC  -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC  the hormonal control of several regulatory proteins including
CC  glycogen synthase, MYB and the transcription factor JUN (By
CC  similarity).
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Monomer. Interacts with NIN (By similarity).
CC  -1- PTM: Phosphorylation on Tyr-216 is necessary for the activity (By
CC  similarity).
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC  subfamily.
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CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
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EMBL; AF156099; AAD39258.2; -; mRNA.
EMBL; BC006936; AAH06936.1; -; mRNA.
EMBL; BC007433; AAH0743.1; -; mRNA.
HSSP; P49841; LGNG.
SMR; Q9WV60; 23-386.
IntAct; Q9WV60; -.
Ensembl; ENSMUSG00000022812; Mus musculus.
MGI; MGI:1861437; Gsk3b.
GO; GO:0005829; C:Cytosol; IDA.
GO; GO:0005634; C:Nucleus; IDA.
GO; GO:008013; F:beta-catenin binding; IPI.
GO; GO:0050321; P:tau-protein kinase activity; IDA.
GO; GO:0006916; P:anti-apoptosis; IMP.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0045444; P:fat cell differentiation; IDA.
GO; GO:0009887; P:organogenesis; IMP.
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
GO; GO:0006611; P:protein-nucleus export; IDA.
GO; GO:0006320; P:entry into mitotic cell cycle; IDA.
GO; GO:0006950; P:response to stress; IDA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_kinase.
InterPro; IPR002290; Ser_thr_kinase.
InterPro; IPR001245; Tyr_kinase.
Pfam; PF00069; Kinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW  Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
FT  CHAIN 1 420 /FTID=PRO_0000085981.
FT  DOMAIN 56 340 protein kinase.
FT  NP_BIND 62 70 ATP (By similarity).
FT  ACT_SITE 181 181 Proton acceptor (By similarity).

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FT BINDING      85      85      ATP (By similarity).
FT MOD_RES      9       9       Phosphoserine (by PKB/AKT1) (By
FT                      similarity).
FT MOD_RES     216     216     Phosphotyrosine.
FT MOD_RES     389     389     Phosphoserine.
FT SEQUENCE    420 AA; 46710 MW; 200C3FD1B38B4883 CRC64;

Query Match      96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRITSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRITSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNI VRLRYFFYSSG 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNI VRLRYFFYSSG 120
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEYVLNLVDYVPETVYRVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLDDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
DB 181 DIKPQNLDDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQKAHP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQKAHP 300
QY 311 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
Q6FI27 HUMAN PRELIMINARY; PRT; 420 AA.
AC Q6FI27;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE GSK3B protein.
GN GSK3B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkwondinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL; CR536510; CAG38748.1; -; mRNA.
CC
CC SMR; O6FI27; 23-386.
CC Ensembl; ENSG0000082701; Homo sapiens.
CC GO; GO:000524; F:ATP binding; IEA.
CC GO; GO:000166; F:nucleotide binding; IEA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Chr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 4ACC24D00CDBB9C3 CRC64;

Query Match      96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRITSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRITSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNI VRLRYFFYSSG 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNI VRLRYFFYSSG 120
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEYVLNLVDYVPETVYRVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLDDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
DB 181 DIKPQNLDDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQKAHP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQKAHP 300
QY 311 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4
Q5KU03 MOUSE PRELIMINARY; PRT; 420 AA.
AC Q5KU03;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Glycogen synthase kinase 3 beta/tau protein kinase I (NOD-derived
DE CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,
DE clone:F630213P21 product:glycogen synthase kinase 3 beta, full insert
DE sequence) (NOD-derived cDNA +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone:F630015008 product:glycogen synthase
DE kinase 3 beta, full insert sequence).
GN Name=Gsk3b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RN NUCLEOTIDE SEQUENCE.
RP Sano Y., Nakano A., Hirai K., Ohta S., Yanagisawa M., Sato S.,
RA Imahori K.;
RT "Glycogen synthase kinase 3b gene: complete genomic and cDNA
RT structures.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard A., Wells K., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Attala R.N., Baile T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Heminger P., Gengler S., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawahara T., Kohjima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=22334683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaado I., Osato I., Saiki R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami T.A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schramm L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y., Hirokawa T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleichmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J., Schramm L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiseunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;



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RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Komura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanishi A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AB066114; BAD6827.1; -; mRNA.
CC EMBL; AK170965; BA42146.1; -; mRNA.
CC EMBL; AK154293; BA32494.1; -; mRNA.
CC SMR; Q5K003; 23-386.
CC DR Ensembl; ENSMUSG0000022812; Mus musculus.
CC MG1; MG1:1861437; Gsk3b.
CC DR GO; GO:0005829; C:cytosol; IDA.
CC DR GO; GO:0005634; C:nucleus; IDA.
CC DR GO; GO:0008013; P:beta-catenin binding; IPI.
CC DR GO; GO:0050321; P:tau-protein kinase activity; IDA.
CC DR GO; GO:0006916; P:anti-apoptosis; IMP.
CC DR GO; GO:0008283; P:cell proliferation; TAS.
CC DR GO; GO:0045444; P:fat cell differentiation; IDA.
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CC Query Match 96.7%; Score 2013; DB 2; Length 420;
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CC Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 VINGSGFVVYQAKLDSGELVAIKKVLQDKRPNRLEQIMRKLDHCNIVRLRYFFYSVG 120
QY 131 EKDEEVYLNVLVDVPTVYRVARHYSRAKQTLPIVIVKLYMQLPSLAYIHSFGICHR 190
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QY 191 DIKPNLLDPTAVLKLCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
DB 181 DIKPNLLDPTAVLKLCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLLGQIPPGSGVDQLVEIKVLGTPTRQIRRMNPNYTFKFPQIKAH 310
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QY 311 WTKVFRPTPEALCSRLLEVTPTARLTPLECAHSFPDELDPNVKHPNGRDTPLF 370
DB 301 WTKVFRPTPEALCSRLLEVTPTARLTPLECAHSFPDELDPNVKHPNGRDTPLF 360
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DB 361 NFFTQELSSNPPLATILIPPHARI 384
RESULT 5
ID GSK3B RAT STANDARD; PRT; 420 AA.
AC P18266;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 61.
DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta) (Factor A)
DE (FA).
GN Name=Gsk3b;

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=90316097; PubMed=2164470;
RA Woodgett J.R.;
RT "Molecular cloning and expression of glycogen synthase kinase-3/factor
RT A.";
RL EMBL J. 9:2431-2438(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=93307488; PubMed=7686508; DOI=10.1016/0014-5793(93)81066-9;
RA Ishiguro K., Shiratsuchi A., Sato S., Omori A., Arioka M.,
RA Kobayashi S., Uchida T., Imahori K.;
RT "Glycogen synthase kinase 3 beta is identical to tau protein kinase I
RT generating several epitopes of paired helical filaments.";
RL FEBS Lett. 325:167-172(1993).
RN [3]
RP PHOSPHORYLATION SITE TYR-216.
RX MEDLINE=93178457; PubMed=8382613;
RA Hughes K., Nikolakaki E., Plyte S.E., Totty N.F., Woodgett J.R.;
RT "Modulation of the glycogen synthase kinase-3 family by tyrosine
RT phosphorylation.";
RL EMBL J. 12:803-808(1993).
CC -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC the hormonal control of several regulatory proteins including
CC glycogen synthase, MYB and the transcription factor JUN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts with NIN (By similarity). Monomer.
CC -1- PTM: Phosphorylation of Tyr-216 is necessary for the activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC subfamily.
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; X53428; CAA37519.1; -; mRNA.
CC EMBL; X73653; CAA52020.1; -; mRNA.
CC PIR; S14708; TYRKB.
CC HSP; P49841; 1109.
CC SMR; P18266; 23-386.
CC DR Ensembl; ENSRNOG00000002833; Rattus norvegicus.
CC RGD; 70982; Gsk3b.
CC DR GO; GO:0004696; F:glycogen synthase kinase 3 activity; IDA.
CC DR GO; GO:0005515; F:protein binding; IDA.
CC DR GO; GO:0030010; P:establishment of cell polarity; IDA.
CC DR GO; GO:0006917; P:induction of apoptosis; IDA.
CC DR GO; GO:0045892; P:negative regulation of transcription, DNA-d. .; IDA.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR008271; Ser Thr pkin AS.
CC DR InterPro; IPR002290; Ser Thr pkinase.
CC DR InterPro; IPR001245; Tyr_pkinase.
CC DR Pfam; PF00069; Pkinase; 1.
CC DR ProDom; PD000001; Prot kinase; 1.
CC DR SMART; SM00220; S_TKc; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
CC Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
CC CHAIN 1 420 Glycogen synthase kinase-3 beta.
CC /FTid=PRO_0000085982.
CC DOMAIN 56 340 Protein kinase.
CC NP_BIND 62 70 ATP (By similarity).
CC ACT_SITE 181 181 Proton acceptor (By similarity).
CC BINDING 85 85 ATP (By similarity).
CC MOD_RES 9 9 Phosphoserine (by PKB/AKT1) (By
CC similarity).

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FT MOD\_RES 216 216 Phosphotyrosine.  
FT MOD\_RES 389 389 Phosphoserine (By similarity).  
FT MUTAGEN 216 216 Y->F: Loss of phosphorylation.  
FT CONFLICT 240 240 M -> V (in Ref. 2).  
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DB 241 WSAGCVLAELLGQPIFGDQVQLVEIKVLGTPTRQIREMNPNTYEFKPPQIKAH 300  
  
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DB 361 NFFTQELSSNPPLATILIPPHARI 384  
  
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AC Q5YJC2;  
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.  
DT 23-NOV-2004, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE Glycogen synthase kinase 3 beta.  
OS Spermophilus citellus (European suslik) (Citellus citellus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Scuridae; Xerinae; Marmotini; Spermophilus.  
OX NCB1\_TaxID=9997;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Stieler J.T., Strijkstra A.M.;  
RT "Molecular cloning of Spermophilus citellus glycogen synthase kinase 3 beta.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AY392021; AAS59774.1; -; mRNA.  
DR SRR; Q5YJC2; 23-386  
DR GO; GO:000524; F:ATP binding; IEA.  
DR GO; GO:000166; F:nucleotide binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
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DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Kinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
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Best Local Similarity 99.5%; Pred. No. 1.5e-147;  
Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 11 MSGRPTTTSFAESCKPVQPSAFGSMKVSRRDQSGKVTTVATPGGQDRPQBSVYTDTK 70  
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DB 301 WTKVFRPTPPPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNRGTDPALF 360  
  
QY 371 NFFTQELSSNPPLATILIPPHARI 394  
DB 361 NFFTQELSSNPPLATILIPPHARI 384  
  
RESULT 7  
Q9IBD2\_BRARE PRELIMINARY; PRT; 421 AA.  
AC Q9IBD2;  
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2000, sequence version 1.  
DT 07-FEB-2006, entry version 26.  
DE Glycogen synthase kinase 3 beta.  
GN Name=gsk3b;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCB1\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;  
RA Shimizu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,  
RA Bae Y.-K., Hibi M., Hirano T.;  
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the  
RT formation of the dorsal organizer in zebrafish.";  
RL Mech. Dev. 91:293-303(2000).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AB032265; BAA92442.1; -; mRNA.  
DR HSSP; P49841; 1109.

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DR SMR; Q91BD2; 23-386.
DR Ensembl; ENSDARG00000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46856 MW; 2B251B4C660C00EB CRC64;

Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 11 MSGRPTTTFAESCKPVQPSAFGSMKVS RDGSKVTTVATPGGDP RPQEVSYTDTK 70
Db 1 MSGRPTTTFAESCKPVQPSAFGSMKVS RDGSKVTTVATPGGDP RPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYPAPELIFGATDYSIDV 250
Db 181 DIKPNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYPAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTPPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTTQELSSNPPLATILIPPHAR 393
Db 361 NFTTQELSSNPPLATILIPPHAR 383

RESULT 8
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ID QYH60;
AC QYH60;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Glycogen synthase kinase 3.
GN Name=gsk3b; Synonyms=GSK3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;

```

```

RT "Differential expression of glycogen synthase kinase 3 genes during
RT zebrafish embryogenesis.";
RL Mech. Dev. 91:387-391(2000).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ223502; CAA11420.1; -; mRNA.
DR HSSP; P49841; 1109.
DR SMR; QYH60; 23-386.
DR Ensembl; ENSDARG00000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46872 MW; 2B251B4C7B6C00EB CRC64;

Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 11 MSGRPTTTFAESCKPVQPSAFGSMKVS RDGSKVTTVATPGGDP RPQEVSYTDTK 70
Db 1 MSGRPTTTFAESCKPVQPSAFGSMKVS RDGSKVTTVATPGGDP RPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYPAPELIFGATDYSIDV 250
Db 181 DIKPNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYPAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTPPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTTQELSSNPPLATILIPPHAR 393
Db 361 NFTTQELSSNPPLATILIPPHAR 383

RESULT 9
QY1757_XENLA PRELIMINARY; PRT; 420 AA.
ID QY1757_XENLA;
AC QY1757;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Intracellular kinase (Xgsk-3 protein).

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GN Name=Xgsk-3;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=95237008; PubMed=7720580;  
 RX Pierce S.B., Kmelman D.;  
 RT "Regulation of Spemann organizer formation by the intracellular kinase  
 RT Xgsk-3".  
 RL Development 121:755-765(1995).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative".  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC ENBL; L38492; AAC42224.1; -; mRNA.  
 DR EMBL; BC108581; AA108582.1; -; mRNA.  
 DR PIR; I51425; I51425.  
 DR HSP; P49841; I109.  
 DR SWR; Q91757; 23-386.  
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 DR GO; GO:0001666; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0004688; F:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser Thr\_pkin AS.  
 DR InterPro; IPR002290; Ser Thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; I.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 420 AA; 46903 MW; C02280B8A35785D CRC64;  
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 Best Local Similarity 95.3%; Pred. No. 1e-141;  
 Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
 QY 11 MSGRPRTTSFAESCKPVQOPSGFSGMKVSRDKGSKVTIVVATPGQGPDRPQEVSYTDTK 70  
 DB 1 MSGRPRTTSFAESCKPVQOPSGFSGMKVSRDKGSKVTIVVATPGQGPDRPQEVSYTDTK 60  
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 DB 61 VINGSGFVVYQAKLDCGSELVAIKVLODRKFNRELIMRKLHCHNIVRLRYFFYSYG 120  
 QY 131 EKDEVYLVLDYVETVYRVARHYHSAKQTLPIVYVKLYMYQLFRSLAYIHSGFICHR 190  
 DB 121 EKDEVYLVLDYVETVYRVARHYHSAKQALPIIYVKLYMYQLFRSLAYIHSGFICHR 180  
 QY 191 DIKPQNLLDPDTAVLKLCDFGSAKQLVRCPEPNVSYICSRYYRAPELIFGATDVTSSIDV 250  
 DB 181 DIKPQNLLDPDTAVLKLCDFGSAKQLVRCPEPNVSYICSRYYRAPELIFGATDVTSSIDV 240  
 QY 251 WSAGCVLAELLLGQPIFGDGSVDQLVEIIVKVLGTPTREQIREMNPNTYEFKPKQIAHP 310  
 DB 241 WSAGCVLAELLLGQPIFGDGSVDQLVEIIVKVLGTPTREQIREMNPNTYEFKPKQIAHP 300  
 QY 311 WTKVFRPTPEAIACSRLLVETPTARLPLACAHSPFDELDPNVKHPNGRDTPALF 370  
 DB 301 WTKVFRPTPEAIACSRLLVETPTARLPLACAHSPFDELDPNVKHPNGRDTPALF 360  
 QY 371 NFTTOELSSNPPLATILIPPHAR 393  
 DB 361 NFTTOELSSNPPLATILIPPHAR 383  
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 Q91627 XENLA  
 ID Q91627 XENLA PRELIMINARY; PRT; 420 AA.  
 AC Q91627;  
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 34.  
 DE Glycogen synthase kinase 3 beta.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=95396823; PubMed=7667318;  
 RA Dominguez I., Itoh K., Sokol S.Y.;  
 RT "Role of glycogen synthase kinase 3 beta as a negative regulator of  
 RT dorsoventral axis formation in Xenopus embryos".  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:8498-8502(1995).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC ENBL; U31862; AAA84444.1; -; mRNA.  
 DR PIR; I51692; I51692.  
 DR HSP; P49841; I109.  
 DR SWR; Q91627; 23-386.  
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 DR GO; GO:0001666; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
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 DR InterPro; IPR008271; Ser\_thr\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-Binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 420 AA; 46900 MW; 4FECEA381835BFC7 CRC64;  
 Query Match 92.4%; Score 1923; DB 2; Length 420;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-141;  
 Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
 QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVSRRDKGSKVTTTVAATPGQGPDRPQEVSYDTDK 70  
 Db 1 MSGRPRTTSPAESCKPVQPSFGSMKVSRRDKGSKVTTTVAATPGQGPDRPQEVSYDTDK 60  
 QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFVSSG 130  
 Db 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFVSSG 120  
 QY 131 EKDEVLNLVLDVVPETVYVVARHYSRAKOTLPVIVYKLYMQLFPSLAYIHSFGICHR 190  
 Db 121 EKXDEVYLVLDVVPETVYVVARHYSRAKQALPIIVYKLYMQLFPSLAYIHSFGICHR 180  
 QY 191 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSYRYAPELIFGATDYSIDV 250  
 Db 181 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSYRYAPELIFGATDYSIDV 240  
 QY 251 WSAGCVLAELLGQIPFGDSGVDDVLEIIVKLGTPTRBOIREMNPNTYEFKFPQIKAH 310  
 Db 241 WSAGCVLAELLGQIPFGDSGVDDVLEIIVKLGTPTRBOIREMNPNTYEFKFPQIKAH 300  
 QY 311 WTKVFRPTPEALCSRLLEVTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPTPEALCSRLLEVTPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360  
 QY 371 NFTQELSSNPPLATILIPHAR 393  
 Db 361 NFTQELSSNPPLATILIPHAR 383

## RESULT 11

Q4S0H0\_TETNG PRELIMINARY; PRT; 496 AA.  
 AC Q4S0H0;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Chromosome 2 SCF14781, whole genome shotgun sequence.  
 GN ORFNames=GSTENG00026022001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthonard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J., Robinson-Rechavi M.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.",  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RG NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 cycle. It is required in higher cells for entry into S-phase and  
 mitosis. Component of the kinase complex that phosphorylates the  
 repetitive C-terminus of RNA polymerase II. Catalytic component of  
 MPF (By similarity).  
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 mature oocytes (By similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; CAA01014781; CAG05862.1; -; Genomic\_DNA.  
 DR SNR; Q4S0H0; 32-133.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-Binding;  
 KW Serine/threonine-protein kinase; Transferase.  
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 Best Local Similarity 73.8%; Pred. No. 6.3e-131;  
 Matches 354; Conservative 8; Mismatches 3; Indels 115; Gaps 3;  
 QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVSRRDKGSKVTTTVAATPGQGPDRP 61  
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 QY 122 LRYFFYSYSGEK----- 132  
 Db 121 LRYFFYSYSGEK----- 130  
 QY 133 -----KDEVLNLVLDYV 145  
 Db 181 PSGNGQKWLRCGRKRSLTFLRESANKRVDIPQVPRSRGHSVRSKDEVLNLVLDYV 240  
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 Db 361 NFTQELSSNPPLATILIPHAR 383

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RESULT 12  
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 AC Q9YH61;  
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 DT 01-MAY-1999, sequence version 1.  
 DT 07-FEB-2006, entry version 38.  
 DE Glycogen synthase kinase 3 alpha.  
 GN Name-gsk3a; Synonyms=GSK3;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;  
 RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;  
 RT "differential expression of glycogen synthase kinase 3 genes during  
 zebrafish embryogenesis.";  
 RL Mech. Dev. 91:387-391(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RG NIH MGC Project;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC EMBL; AJ223501; CAA11419.1; -; mRNA.  
 CC EMBL; BC056332; AAH56332.1; -; mRNA.

DR EMBL; BC065952; AAH65952.1; -; mRNA.  
 DR HSSP; P49841; 1Q3W.  
 DR SMR; Q9YH61; 52-412.  
 DR Ensembl; ENSDARG00000015681; Danio rerio.  
 DR ZFIN; ZDB-GENE-990714-3; gsk3a.  
 DR CO; CO:0005524; F:ATP binding; IEA.  
 DR CO; CO:0000166; F:nucleotide binding; IEA.  
 DR CO; CO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR CO; CO:0016740; F:transferase activity; IEA.  
 DR CO; CO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; prot kinase.  
 DR InterPro; IPR008271; Ser Thr\_kin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 440 AA; 48065 MW; 66A8E8D070ACA093 CRC64;  
 Query Match 81.9%; Score 1704.5; DB 2; Length 440;  
 Best Local Similarity 79.1%; Pred. No. 4.7e-124;  
 Matches 326; Conservative 26; Mismatches 25; Indels 35; Gaps 3;  
 QY 12 SGRPTTTSFAESCKPVQQP-----SAFGSMKVSRD 41  
 Db 4 SGRPTTSSFAE---PGVFGAAAAAGSAVAGSSSGKGTGGAQAGSSSGFGNKLGR - 59  
 QY 42 KDGSKVTTVVATPGQGPDRPQEVSYTDTKIVGNSGFGVYQAKLDCSGELVAIKKVLQDK 101  
 Db 60 -DSGKVTTVVATPGQGPDRPQEVSYTDTKIVGNSGFGVYQARLDSQEMVAIKKVLQDK 118  
 QY 102 RFKNRELQIMRKLDHCNIVRLRYFFYSKGEKDEVLNLDVVPVTVVVAHYHRAKQ 161  
 Db 119 RFKNRELQIMRKLDHCNIVRLRYFFYSKGEKDEVLNLDVVPVTVVVAHYHFNKSKT 178  
 QY 162 TLPIVIVKLYVMYQFRLSLAYIHSFGICHRDIPQNLDDPDTAVLKLCDFGSAKQLVRGE 221  
 Db 179 TIPIIVKVMYQFRLSLAYIHSQGVCHRIDIPQNLDDPDTAVLKLCDFGSAKQLVRGE 238  
 QY 222 PNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLIGQIFPGDSGVQDLVEIK 281  
 Db 239 PNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLIGQIFPGDSGVQDLVEIK 298  
 QY 282 VLGTPTREQIREMNPNTYEFKFPQIKAHPTWKVFRPTTPPEAIALCSRLLEYTPTARLTP 341  
 Db 299 VLGTPTREQIREMNPNTYEFKFPQIKAHPTWKVFRPTTPPEAIALCSRLLEYTPTARLTP 358  
 QY 342 LEACAHGFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 393  
 Db 359 LEACAHGFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 410

RESULT 13  
 Q9IBD3\_BRARE  
 ID Q9IBD3\_BRARE PRELIMINARY; PRT; 435 AA.  
 AC Q9IBD3;  
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 26.  
 DE Glycogen synthase kinase 3 alpha.  
 GN Name-gsk3a;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.



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RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RA Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Iabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; A3032264; BAA92441.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9IBD3; 52-412.
DR Ensembl; ENSDARG00000015681; Danio rerio.
DR ZFIN; ZDB-GENE-990714-3; gsk3a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkin AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00111; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 435 AA; 47791 MW; ED7793A03D8C706 CRC64;

Query Match 80.2%; Score 1669.5; DB 2; Length 435;
Best Local Similarity 78.2%; Pred. No. 2.4e-121;
Matches 322; Conservative 26; Mismatches 29; Indels 35; Gaps 3;

QY 12 SGRPRTTSFAESCKPVQQP-----SAPGSMKVSRD 41
DB 4 SGRPRTSSPAE---PPQVPGAAAAAGSAVAGSSSGKTGGAQAGSGSSGFGNLKGR- 59

QY 42 KDGSKTTVVATGQGPDRPQEVSYTDTKVIKNGSGFVYQAKLDCSGELVAIKVLQDK 101
DB 60 -DSGKTTVVATGQGPDRPQEVSYTDTKVIKNGSGFVYQAKLDCSGELVAIKVLQDK 118

QY 102 RFKNRELQIMRKLDHCNIVLRIFYFFSYSGEKDEVLNVLVDYVPETVYVARHYSRAKQ 161
DB 119 RFKNRELQIMRKLDHCNIVLRIFYFFSYSGEKDEVLNVLVDYVPETVYVARHYSRAKQ 178

QY 162 TLPVIYVKLYMYQLFRSLAYHSFGICHRDIPKPNLLDPDTAVLKLDCFGSAKQLVRGE 221
DB 179 TILPIYVKVYMYQLFRSLAYHSFGICHRDIPKPNLLDPDTAVLKLDCFGSAKQLVRGE 238

QY 222 PNVSYICSRYPAPLIFGATDTSIDWSACVLAELLGQPIPGSGVDOLVEIHK 281
DB 239 PNVSYICSRYPAPLIFGATDTSIDWSACVLAELLGQPIPGSGVDOLVEIHK 298

QY 282 VLGTPTREQIREMNPNTPEKFPQIKAHPTKVFRTPEALCSRLLEYTPPTARLTP 341
DB 299 VLGPXTREQIREMNPNTPEKFPQIKAHPTKVFRTPEALCSRLLEYTPPTARLTP 358

QY 342 LEACAHFFDELDPNVKHPNGRDTPALFNPFTTQELSSNPPLATILIPPHAR 393
DB 359 LEACAHFAFFDELKXXNARLNGRELPOLFNFSFVLSIQPLNSILIPPHAR 410

RESULT 14
Q9NL43 CIOIN
ID Q9NL43_CIOIN PRELIMINARY; PRT; 407 AA.
AC Q9NL43;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

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DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 32.
DE Glycogen synthase kinase alpha/beta.
GN Name=CiGSK; Synonyms=Ci-GSK alpha/beta;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Imai K., Takada N., Satoh N., Satou Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16252120; DOI=10.1007/s00427-005-0016-9;
RA Satou Y., Satoh N.;
RT "Cataloging transcription factor and major signaling molecule genes
RT for functional genomic studies in Ciona intestinalis.";
RL Dev. Genes Evol. 215:580-596(2005).
CC -----
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CC -----
DR EMBL; AB031544; BAA92186.1; -; mRNA.
DR EMBL; AB211133; BAE06824.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9NL43; 9-368.
DR Ensembl; ENSCING000000001821; Ciona intestinalis.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 407 AA; 45566 MW; E71594A9B6B59F10 CRC64;

Query Match 80.1%; Score 1666.5; DB 2; Length 407;
Best Local Similarity 83.0%; Pred. No. 3.8e-121;
Matches 318; Conservative 24; Mismatches 26; Indels 15; Gaps 2;

QY 11 MSGRPRTTSFAESCKPVQQPSPAFSGMKVSRDKDGSKVTWATPGQGPDRPQEVSYTDTK 70
DB 1 MGAAPKTT-----LGNMKGSRDKE-SKITTVVATHGHPDRPQEVAYTDTK 45

QY 71 VIGNGSGFVYQAKLDCSGELVAIKVLQDKRFKNRELQIMRKLDHCNIVLRIFYPSG 130
DB 46 VIGNGSGFVYQARLIESNEWAIKKVLQDKRFKNRELQIMRKLDHCNIVLRIFYPSG 105

QY 131 EKDEVLNVLVDYVPETVYVARHYSRAKQITPLVYVKLYMYQLFRSLAYHSFGICHR 190
DB 106 DKDEIYLNVLVDYVPETVYVARQYSSKQITPLVYVKLYMYQLFRSLAYHSFGICHR 165

QY 191 DIKPNLLDPDTAVLKLDCFGSAKQLVRGEPNVSYICSRYPAPLIFGATDTSIDV 250
DB 166 DIKPNLLDPDTAVLKLDCFGSAKQLVRGEPNVSYICSRYPAPLIFGATDTSIDV 225

QY 251 WSAGCVLAELLGQPIPGSGVDOLVEIHKVLGTPTREQIREMNPNTPEKFPQIKAH 310
DB 226 WSAGCVLAELLGQPIPGSGVDOLVEIHKVLGTPTREQIREMNPNTPEKFPQIKAH 285

QY 311 WTKVFRPRTPEALCSRLLEYTPPTARLTPLEACAHSEFDELDPNVKHPNGRDTPALF 370
DB 286 WSKVFRPRTPEALCSRLLEYTPPNRISPLESCAHSEFDELRLPNTKLPNGRSPLPLF 345

QY 371 NFFTQELSSNPPLATILIPPHAR 393

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Db	346	NFTDKELSIKSPNNLLIPHAR	368	:
RESULT 15				
Q6UGS	LYTVA			
ID	Q6UGS_LYTVA	PRELIMINARY;	PRT;	414 AA.
AC	Q6UGS;			
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.		
DT	05-JUL-2004,	sequence version 1.		
DT	07-FEB-2006,	entry version 14.		
Qy	252	SAGCVLAELLGQPIFPGDSGVDDQLVEIIKVLGTFTREQIRKEMNNNYTFEPQIKAPHW	311	:
Db	242	SAGCVLAELLGQPIFPGDSGVDDQLVEIIKVLGTFTREQIRKEMNNNYTFEPQIKAPHW	301	:
Qy	312	TKVFRPRTTPEAIALCSRLLEYTPPTARLTPLACAHSPFDELDRDNVKNPGRDTPPALFN	371	:
Db	302	SKVFRTRTPADAIQLCSRLLEYTPKSRIKPLEACAHQFSELRDPGIIKLNGRELPLFN	361	:
Qy	372	FTTQELSSNPPLATILIPPH	391	:
Db	362	FTAGELASKPSLRTALIPPH	381	:

[illegible]

Query Match	78.4%;	Score 1632;	DB 2;	Length 414;
Best Local Similarity	80.5%;	Pred. No. 1.9e-118;		
Matches 306;	Conservative 35;	Mismatches 37;	Indels 2;	Gaps 1;
QY	12	SGRPRTTSAESCKPVQOQSAFGSMKVSVDKDGSKVTTVWATPGQDPDRPOEVSVTDTKV	71	
DB	4	SGRPRTTSPADNR--GSTSSYGGIKVSRDKDSSKITSVTATEGPPDPRTKEISYTTTRV	61	
QY	72	INGSGFVVYQAKLDCSGBELVAIKKVLQDQRFKNRELOIMRKLDCNTRVRLRYFFYSGE	131	
DB	62	INGSGFVVYQARVMDTNDLVAIKKVLQDQRFKNRELOIMRRLDHNNIVKLKYFFYSGE	121	
QY	132	KXDEVYLNVLVDYVPETVYRVARHYSRAKOTLPVIYVKLYMYQLFRSLAYTHSFGICHRD	191	
DB	122	KXDEVYLNVLVEYVPETVYRVARHYSKAKQITISLYVKLYMYQLFRSLAYTHSMGICHRD	181	
QY	192	IKPQNLLLPDPTAVLKLCDPFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVW	251	
DB	182	IKPQNLLNPETAVLKLCDPFGSAKVLVRGEPNVSYICSRYYRAPELIFGATDYTCDIDVW	241	

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:03:15 ; Search time 195 Seconds  
(without alignments)  
923.812 Million cell updates/sec

Title: US-10-733-816-2  
Perfect score: 2081  
Sequence: 1 MEVPMEGGMSGRPTTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	5	Abb07578 Human tru
2	2024	97.3	420	4	Aae05998 Human gly
3	2024	97.3	420	5	Abb07577 Human gly
4	2024	97.3	420	7	AbR44294 Human gly
5	2024	97.3	420	7	Adk11467 Human gly
6	2024	97.3	420	8	Adh09637 Human hos
7	2024	97.3	420	8	AdR40191 Human gly
8	2024	97.3	420	8	AdS92965 Glycogen
9	2024	97.3	420	8	AdT92555 Human gly
10	2013	96.7	414	8	AdR06333 p38-alpha
11	2013	96.7	420	2	AR61327 Tau-prote
12	2013	96.7	420	5	Abb77875 Amino aci
13	2013	96.7	420	6	Abp70714 Human gly
14	2013	96.7	420	7	AbR44293 Human gly
15	2013	96.7	420	7	AdD68742 Rat tau p
16	2013	96.7	420	7	AdE64053 Human Pro
17	2013	96.7	420	8	Adh09634 Human hos
18	2013	96.7	420	8	AdR06320 Gsk-3 bet
19	2013	96.7	420	8	AdR06317 Gsk-3 bet
20	2013	96.7	420	9	AdY64106 Human gly
21	2013	96.7	420	9	AEA39562 Human gly
22	2013	96.7	420	9	AEA39564 Mouse gly
23	2013	96.7	420	9	Aeb28124 Human gly

24	2013	96.7	420	9	AEC81932	Human gly
25	2013	96.7	420	9	AEE06398	Glycogen
26	2013	96.7	428	7	ADC50594	Human tau
27	2010	96.6	420	2	AAR61326	Tau-prote
28	2010	96.6	420	6	ABR82106	Human gly
29	2010	96.6	420	7	ABR44289	Human gly
30	2010	96.6	420	7	ADE64051	Rat Prote
31	2010	96.6	420	8	ADI28893	Mouse gly
32	1996.5	95.9	433	7	ABR44295	Human gly
33	1996.5	95.9	433	7	ABR44298	Human gly
34	1996.5	95.9	433	7	ADJ69554	Human hea
35	1996.5	95.9	433	8	ADH09633	Human hos
36	1996.5	95.9	433	8	ADO49107	Human ded
37	1996.5	95.9	433	8	ADU20919	Human gly
38	1996.5	95.9	433	8	ADU06409	Novel bro
39	1996.5	95.9	433	9	AEB25735	Human and
40	1996.5	95.9	433	9	AEC34201	Human GSK
41	1996.5	95.9	433	9	AEE06396	Glycogen
42	1996.5	95.9	439	8	ADR66057	Human pro
43	1994.5	95.8	439	8	ADR66399	Human pro
44	1978	95.1	385	9	ADY85481	Catalytic
45	1919	92.2	387	9	AEE06402	Glycogen

#### ALIGNMENTS

RESULT 1  
ABB07578  
ID ABB07578 standard; protein; 394 AA.  
XX  
AC ABB07578;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human truncated GSK3beta polypeptide 557.  
XX  
KW GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human;  
KW Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FT Peptide I..10  
FT Peptide /note= "Glu-tag and Gly linker"  
FT Peptide 11..394  
XX  
XX /note= "truncated GSK3beta"  
XX  
XX WO200210357-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 25-JUL-2001; 2001WO-US023539.  
XX  
XX 27-JUL-2000; 2000US-0221242P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY;  
XX Coit DG, Nguyen SH, Medina-Selby A;  
XX WPI; 2002-189732/24.  
XX  
XX New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids  
XX encoding them, useful for treating diseases mediated by GSK3 activity,  
XX including Alzheimer's disease, type 2 diabetes and inflammation.  
XX  
XX Claim 8; Fig 2A-B; 36pp; English.  
XX  
XX The invention provides glycogen synthase kinase 3 (GSK3) polypeptides  
XX capable of crystallisation, including GSK3alpha and GSK3beta  
XX polypeptides. The GSK polypeptides can be used to identify and optimise  
XX GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as

CC pharmaceutical agents, for treating diseases mediated by GSK3 activity,  
 CC including Alzheimer's disease, type 2 diabetes and inflammation. The  
 CC present sequence represents the amino acid sequence of a truncated  
 CC GSK3beta polypeptide 557  
 XX  
 SQ Sequence 394 AA;  
 Query Match 100.0%; Score 2081; DB 5; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-216;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEYMPMGSGGSGRPTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDR 60  
 DB 1 MEYMPMGSGGSGRPTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDR 60  
 QY 61 PQEVSYTDTKVINGSGFGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLHCNIV 120  
 DB 61 PQEVSYTDTKVINGSGFGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLHCNIV 120  
 QY 121 RLRYFFSYSGGKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180  
 DB 121 RLRYFFSYSGGKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180  
 QY 181 YIHSFGICHRDIKQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFG 240  
 DB 181 YIHSFGICHRDIKQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFG 240  
 QY 241 ATDYTSIDVMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLTPTREQIREMNPYTE 300  
 DB 241 ATDYTSIDVMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLTPTREQIREMNPYTE 300  
 QY 301 FKFPQIKAHPMTKVFRPTPEALCSRLLEYTPARLTPLCAHSPFDELDPNVKH 360  
 DB 301 FKFPQIKAHPMTKVFRPTPEALCSRLLEYTPARLTPLCAHSPFDELDPNVKH 360  
 QY 361 PNGRDTALFNFTTQELSSNPPLATILIPPHARI 394  
 DB 361 PNGRDTALFNFTTQELSSNPPLATILIPPHARI 394  
 RESULT 2  
 AA05998  
 ID AA05998 standard; protein; 420 AA.  
 XX  
 AC AA05998;  
 XX  
 DT 24-SEP-2001 (first entry)  
 XX  
 DE Human glycogen synthase kinase 3-beta #1.  
 XX  
 KW Antisense; glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;  
 KW insulin regulation disorder; neurological disorder; Alzheimer's disease;  
 KW bipolar illness; inflammation; tumour; tau protein kinase I; TPK-1;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200152862-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US001085.  
 XX  
 PR 19-JAN-2000; 2000US-00489765.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Butler MM, McKay R, Monia BP, Wyatt JR;  
 XX  
 DR WPI; 2001-457510/49.  
 DR N-PSDB; AAD11491.  
 XX  
 PT Novel antisense compounds, particularly antisense oligonucleotides for

PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for  
 PT diagnosing, treating neurological and insulin regulation disorders.  
 XX  
 PS Example 13; Page 88-90; 106pp; English.  
 XX

CC The invention relates to antisense compounds targetted to nucleic acid  
 CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau  
 CC protein kinase I (TPK-I)). The antisense compound is useful for  
 CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in  
 CC cells or tissues and for treating diseases or conditions associated with  
 CC the enzyme such as insulin regulation disorder, in particular diabetes  
 CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.  
 CC The antisense compound is also useful for diagnosing diseases associated  
 CC with the expression of glycogen synthase kinase 3-beta and for  
 CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour  
 CC formation and as a research reagent. The present sequence is human  
 CC glycogen synthase kinase 3-beta  
 XX

SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 4; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 5e-210;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 MSGRPRTTSPAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDRPQBSVYTDK 70  
 DB 1 MSGRPRTTSPAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDRPQBSVYTDK 60  
 QY 71 VINGSGFGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFSYSSG 130  
 DB 61 VINGSGFGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFSYSSG 120  
 QY 131 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190  
 DB 121 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180  
 QY 191 DIRPQNLLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
 DB 181 DIRPQNLLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
 QY 251 WSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLTPTREQIREMNPYTEFKFPQIKAH 310  
 DB 241 WSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLTPTREQIREMNPYTEFKFPQIKAH 300  
 QY 311 WTKVFRPTPEALCSRLLEYTPARLTPLCAHSPFDELDPNVKHDPNGRDTALF 370  
 DB 301 WTKVFRPTPEALCSRLLEYTPARLTPLCAHSPFDELDPNVKHDPNGRDTALF 360  
 QY 371 NFFTQELSSNPPLATILIPPHARI 394  
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3

ABB07577

ID ABB07577 standard; protein; 420 AA.

XX

AC ABB07577;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human glycogen synthase kinase 3beta (GSK3beta) polypeptide.

XX

KW GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; neurotic; human;  
 KW Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Modified-site 216

FT /note= "phosphorylated"

FT Peptide 250..419

FT /note= "specifically claimed fragment"

FT Peptide 278..419  
FT /note= "specifically claimed fragment"  
FT Peptide 285..384  
FT /note= "specifically claimed fragment"  
FT Peptide 351..384  
FT /note= "specifically claimed fragment"  
XX  
PN WO200210357-A2.  
XX  
XX  
PD 07-FEB-2002.  
XX  
XX 25-JUL-2001; 2001WO-US023539.  
XX  
XX 27-JUL-2000; 2000US-0221242P.  
PR  
XX (CHIR ) CHIRON CORP.  
XX  
XX Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY;  
PI Coit DG, Nguyen SH, Medina-Selby A;  
XX  
XX WPI; 2002-188732/24.  
XX  
XX New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids  
PT encoding them, useful for treating diseases mediated by GSK3 activity,  
PT including Alzheimer's disease, type 2 diabetes and inflammation.  
XX  
XX Claim 6; Fig 1A-B; 36pp; English.  
XX  
XX The invention provides glycogen synthase kinase 3 (GSK3) polypeptides  
CC capable of crystallisation, including GSK3alpha and GSK3beta  
CC polypeptides. The GSK polypeptides can be used to identify and optimise  
CC GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as  
CC pharmaceutical agents, for treating diseases mediated by GSK3 activity,  
CC including Alzheimer's disease, type 2 diabetes and inflammation. The  
CC present sequence represents the amino acid sequence of human GSK3beta  
CC polypeptide  
XX  
XX  
SQ Sequence 420 AA;  
Query Match 97.3%; Score 2024; DB 5; Length 420;  
Best Local Similarity 100.0%; Pred. No. 5e-210;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKSGKVTTVVATPGQGPDRPQEVSYDTDK 70  
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKSGKVTTVVATPGQGPDRPQEVSYDTDK 60  
Qy 71 VIGNSGFVVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 130  
Db 61 VIGNSGFVVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 120  
Qy 131 EKDEVVYLVLDVVPETVYVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190  
Db 121 EKDEVVYLVLDVVPETVYVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180  
Qy 191 DIKPNLLDPDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 250  
Db 181 DIKPNLLDPDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 240  
Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIRENNPNYTFEKFQIKAHP 310  
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIRENNPNYTFEKFQIKAHP 300  
Qy 311 WTKVFRPTTPEALCSRLLEYTPPTARLTPEACAHSFDPDELDPNVKHPNGRDTPALF 370  
Db 301 WTKVFRPTTPEALCSRLLEYTPPTARLTPEACAHSFDPDELDPNVKHPNGRDTPALF 360  
Qy 371 NFFTQELSSNPPLATILIPPHARI 394  
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4

ABR44294  
ID ABR44294 standard; protein; 420 AA.  
XX  
AC ABR44294;  
XX  
DT 18-AUG-2003 (first entry)  
XX  
DE Human glycogen synthase kinase-3 (GSK3)beta polypeptide.  
XX  
XX GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;  
XX KW vulnery; antiarteriosclerotic; GSK3beta; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN WO2003038037-A2.  
XX  
XX 08-MAY-2003.  
PD  
XX 23-OCT-2002; 2002WO-US033909.  
PF  
XX 29-OCT-2001; 2001US-0350160P.  
PR  
XX 13-NOV-2001; 2001US-0337905P.  
XX  
XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.  
PA  
XX Walsh K;  
PI  
XX WPI; 2003-482140/45.  
XX  
XX Modulating angiogenesis, useful for treating hyperlipidemia, comprises  
PT administering an angiogenesis inhibitor/promoter, such as an  
PT active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3  
PT activator/inhibitor.  
XX  
XX Disclosure; Page 100-101; 115pp; English.  
XX  
XX The invention relates to inhibiting/enhancing angiogenesis. The method  
CC involves administering to a subject needing the treatment, an  
CC angiogenesis inhibitor/promoter, such as an active/inactive glycogen  
CC synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,  
CC where the angiogenesis modulator is administered to inhibit/enhance  
CC angiogenesis in a subject. The methods are useful for treating a  
CC condition associated with increased apoptotic cell death of vascular  
CC endothelial cells, where the condition is characterized by lesion of  
CC blood vessel wall, such as hyperlipidemia, also in the treatment of  
CC myocardial infarction and in the promotion of wound healing. The present  
CC sequence represents a human GSK3beta polypeptide (GenBank Accession No.  
CC S53324)  
XX  
SQ Sequence 420 AA;  
Query Match 97.3%; Score 2024; DB 7; Length 420;  
Best Local Similarity 100.0%; Pred. No. 5e-210;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKSGKVTTVVATPGQGPDRPQEVSYDTDK 70  
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKSGKVTTVVATPGQGPDRPQEVSYDTDK 60  
Qy 71 VIGNSGFVVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 130  
Db 61 VIGNSGFVVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 120  
Qy 131 EKDEVVYLVLDVVPETVYVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190  
Db 121 EKDEVVYLVLDVVPETVYVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180  
Qy 191 DIKPNLLDPDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 250  
Db 181 DIKPNLLDPDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 240  
Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIRENNPNYTFEKFQIKAHP 310

Db 241 WSAGCVLAELLGQPIPPGSDGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKPPQIKAH 300  
 Qy 311 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360  
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 5  
 ADK11467  
 ID ADK11467 standard; protein; 420 AA.  
 AC ADK11467;  
 DT 06-MAY-2004 (first entry)  
 XX Human glycogen synthase kinase 3 beta protein.  
 DE  
 XX cytosolic; cardiovascular; immunosuppressive; nephrotropic;  
 KW antirheumatic; antiarthritic; dermatological; antipsoriatic;  
 KW antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;  
 KW cardiovascular disorder; autoimmune disease; glomerulonephritis;  
 KW rheumatoid arthritis; dermatological disorder; psoriasis;  
 KW inflammatory disorder; malaria; emphysema; alopecia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0203040301-A2.  
 XX  
 XX 15-MAY-2003.  
 XX  
 XX 23-OCT-2002; 2002WO-GB004780.  
 XX  
 XX 05-NOV-2001; 2001GB-00026506.  
 XX 27-NOV-2001; 2001GB-00028384.  
 XX 11-FEB-2002; 2002GB-00003185.  
 XX (CYCL-) CYCLACEL LTD.  
 XX  
 XX Deak P, Frenz L, Glover D, Midgley C;  
 XX WPI; 2003-441540/41.  
 XX N-PSDB; ADK11466.  
 XX  
 XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,  
 XX preventing and/or treating disorders, such as cancer, glomerulonephritis,  
 XX rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.  
 XX  
 XX Example 27; Page 218; 265pp; English.

The invention relates to novel Drosophila species DNA sequences and their encoded proteins with their corresponding human homologues. The proteins or their encoding polynucleotides are useful in a method of prevention, treatment or diagnosis of a disease in an individual, and used to identify a substance capable of binding to the polypeptide or modulating the function of the polypeptide comprising incubating the polypeptide with a candidate substance and determining whether the substance binds to the polypeptide. The compositions are administered to an individual in need of such treatment. The method of diagnosis, in which the presence or absence of a polynucleotide is detected in a biological sample, comprises brining the biological sample containing the nucleic acid such as DNA or RNA into contact with a probe comprising a fragment of at least 15 nucleotides of the polynucleotide, and detecting any duplex formed between the probe and nucleic acid in the sample. The method also comprises providing an antibody capable of binding to the polypeptide, incubating a biological sample with the antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex comprising the antibody is formed. The disease comprises a proliferative disease such as cancer. The antibody or identified substance is also useful in inhibiting the function of a polypeptide

CC and/or regulating a cell division cycle function. The diseases also  
 CC include cardiovascular disorders, autoimmune diseases such as  
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders  
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as  
 CC malaria, emphysema and alopecia. This sequence represents a human homolg  
 CC for one of the Drosophila proteins of the invention.  
 XX  
 SQ Sequence 420 AA;  
 Query Match 97.3%; Score 2024; DB 7; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 5e-210;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 MSGRPRTTFAESCKPVQPSAFSGSMKVSRDKDGSKVTTVATPGQDPDPQEVSYDTK 70  
 Db 1 MSGRPRTTFAESCKPVQPSAFSGSMKVSRDKDGSKVTTVATPGQDPDPQEVSYDTK 60  
 Qy 71 VINGSGFVVYQAKLCDSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFYS 130  
 Db 61 VINGSGFVVYQAKLCDSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFYS 120  
 Qy 131 EKXDEVYLVLDYVPETVVRVARYHYSRAKQTLPVIVYKLYMYQLFRSLAYIHSFGICHR 190  
 Db 121 EKXDEVYLVLDYVPETVVRVARYHYSRAKQTLPVIVYKLYMYQLFRSLAYIHSFGICHR 180  
 Qy 191 DIKPNLLDPTFAVLKLCDFGSAKQVLRGEPNVSYCSRYYPAPELIFGATDYTSSIDV 250  
 Db 181 DIKPNLLDPTFAVLKLCDFGSAKQVLRGEPNVSYCSRYYPAPELIFGATDYTSSIDV 240  
 Qy 251 WSAGCVLAELLGQPIPPGSDGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKPPQIKAH 310  
 Db 241 WSAGCVLAELLGQPIPPGSDGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKPPQIKAH 300  
 Qy 311 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360  
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 6  
 ADH09637  
 ID ADH09637 standard; protein; 420 AA.  
 AC ADH09637;  
 XX  
 XX 11-MAR-2004 (first entry)  
 XX  
 XX Human host factor protein, SEQ ID No 165.  
 XX  
 XX antiviral; host factor; retrovirus; HIV; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W02003094847-A2.  
 XX  
 XX 20-NOV-2003.  
 XX  
 XX 07-MAY-2003; 2003WO-US014382.  
 XX  
 XX 07-MAY-2002; 2002US-0378711P.  
 XX (UYEM-) UNIV EMORY.  
 XX Devine SE;  
 XX WPI; 2004-011998/01.  
 XX  
 XX Identifying an antiviral compound useful for treating HIV comprises  
 XX exposing a cell that expresses a host factor to a candidate compound to  
 XX identify an agent that inhibits the expression or activity of the host

PT factor.  
XX Claim 13; SEQ ID NO 165; 141pp; English.  
XX  
XX  
CC The invention relates to a novel method for identifying an antiviral  
CC compound. The novel method comprises exposing a cell that expresses a  
CC host factor to a candidate compound to identify an agent that inhibits  
CC the expression or activity of the host factor. The novel method involves  
CC identifying an antiviral compound, comprising exposing a first cell that  
CC expresses a host factor to a candidate compound, determining whether the  
CC candidate compound inhibits the expression or activity of the host factor  
CC in the first cell, where a candidate compound that inhibits the  
CC expression or activity of the host factor in the first cell is a  
CC potential antiviral compound, exposing a second cell to the potential  
CC antiviral compound and a retrovirus, and determining whether the compound  
CC inhibits the ability of the retrovirus to infect or replicate within the  
CC second cell, where a potential antiviral compound that inhibits the  
CC ability of the retrovirus to infect the second cell is an antiviral  
CC compound. The method is useful in identifying antiviral agents, including  
CC those that are effective against retroviruses, such as HIV. This sequence  
CC represents a human host factor protein used in the antiviral  
CC identification method of the invention.  
XX  
XX  
SQ Sequence 420 AA;  
  
Query Match 97.3%; Score 2024; DB 8; Length 420;  
Best Local Similarity 100.0%; Pred. No. 5e-210;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 MSGRPRTTSAESCKPVQPSAFSGSMKVSRLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 70  
DB 1 MSGRPRTTSAESCKPVQPSAFSGSMKVSRLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 60  
  
QY 71 VINGSGVGVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 130  
DB 61 VINGSGVGVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
  
QY 131 EKDEVLNLVLDYVPETVYRVARHYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190  
DB 121 EKDEVLNLVLDYVPETVYRVARHYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180  
  
QY 191 DIKPNQLLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250  
DB 181 DIKPNQLLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240  
  
QY 251 WSAGCVLAELLLGQIPFGDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310  
DB 241 WSAGCVLAELLLGQIPFGDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300  
  
QY 311 WTKVFRPRTPEAIALCSRLLEVTPPTARLTPLCAHSHFFDELDPNVKHPNGRDTPLF 370  
DB 301 WTKVFRPRTPEAIALCSRLLEVTPPTARLTPLCAHSHFFDELDPNVKHPNGRDTPLF 360  
  
QY 371 NFTTQELSSNPPLATILIPPHARI 394  
DB 361 NFTTQELSSNPPLATILIPPHARI 384  
  
RESULT 7  
ADRA40191  
ID ADR40191 standard; protein; 420 AA.  
XX  
AC ADR40191;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human glycogen synthase kinase 3 beta (GSK3beta) (1521) protein.  
XX  
KW haematological; cytostatic; erythroid; anaemia; erythrocytosis;  
KW bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;  
KW T-cells; neutropenia; gene therapy; human;  
KW glycogen synthase kinase 3 beta; GSK3beta; enzyme.  
XX

OS Homo sapiens.  
XX WO2004072242-A2.  
XX  
XX 26-AUG-2004.  
XX  
XX 05-FEB-2004; 2004WO-US003417.  
XX  
XX 05-FEB-2003; 2003US-0445241P.  
XX 18-FEB-2003; 2003US-0448389P.  
XX 20-MAR-2003; 2003US-0456320P.  
XX 03-APR-2003; 2003US-0460279P.  
XX 28-APR-2003; 2003US-0465924P.  
XX 13-MAY-2003; 2003US-0470052P.  
XX 26-AUG-2003; 2003US-0498106P.  
XX 04-SEP-2003; 2003US-0500179P.  
XX 15-SEP-2003; 2003US-0502909P.  
XX 10-OCT-2003; 2003US-0510351P.  
XX 17-OCT-2003; 2003US-0512380P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Kelly LM, Carroll JM, Farlow D, Healy A;  
XX  
XX WPI; 2004-625850/60.  
XX N-PSDB; ADR40190.  
XX  
XX Identifying a compound capable of treating a hematological disorder  
XX comprises combining a compound to be tested with a polypeptide related  
XX with the disorder under conditions suitable for binding of the test  
XX compound to the polypeptide.  
XX  
XX Claim 1; SEQ ID NO 72; 321pp; English.  
XX  
XX The invention relates to a novel method for identifying a compound  
XX capable of treating a haematological disorder which comprises combining a  
XX compound to be tested with a specific polypeptide under conditions  
XX suitable for binding of the test compound to the polypeptide. The method  
XX of the invention has haematological and cytostatic applications and may  
XX be useful for identifying compounds for treating a haematological  
XX disorder associated with erythroid cells e.g. anaemia and erythrocytosis,  
XX bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and  
XX thrombosis or B-cells and T-cells e.g. neutropenia. The compounds  
XX identified may be utilised during gene therapy procedures. The current  
XX sequence is that of a human haematological disorder-related protein of  
XX the invention.  
XX  
XX Sequence 420 AA;  
  
Query Match 97.3%; Score 2024; DB 8; Length 420;  
Best Local Similarity 100.0%; Pred. No. 5e-210;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 MSGRPRTTSAESCKPVQPSAFSGSMKVSRLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 70  
DB 1 MSGRPRTTSAESCKPVQPSAFSGSMKVSRLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 60  
  
QY 71 VINGSGVGVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 130  
DB 61 VINGSGVGVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLHCNIVRLRYFFYSYG 120  
  
QY 131 EKDEVLNLVLDYVPETVYRVARHYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190  
DB 121 EKDEVLNLVLDYVPETVYRVARHYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180  
  
QY 191 DIKPNQLLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250  
DB 181 DIKPNQLLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240  
  
QY 251 WSAGCVLAELLLGQIPFGDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310  
DB 241 WSAGCVLAELLLGQIPFGDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300



QY 311 WTKVFRPTTPEAIALCSRLLEYTPARTLTPLECAHSPFDELDRDNNVHPNGRDTPALF 370  
 DB 301 WTKVFRPTTPEAIALCSRLLEYTPARTLTPLECAHSPFDELDRDNNVHPNGRDTPALF 360  
 QY 371 NFFTQELSSNPPLATILIPPHARI 394  
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 8  
 ADS92965  
 ID ADS92965 standard; protein; 420 AA.  
 XX AC ADS92965;  
 XX 02-DEC-2004 (first entry)  
 DE Glycogen synthase kinase 3 beta.  
 XX cytostatic; gene therapy; human;  
 KW branching morphogenesis modulating agent; MBM agent.  
 KW  
 XX Homo sapiens.  
 OS  
 PN WO2004037990-A2.  
 XX 06-MAY-2004.  
 XX 22-OCT-2003; 2003WO-US033549.  
 XX 23-OCT-2002; 2002US-0420554P.  
 PR 30-DEC-2002; 2002US-0436941P.  
 XX  
 PA (EXEL-) EXELIXIS INC.  
 XX Plowman GD, Karim FD, Swimmer C, Habeck HA, Koblizek TI;  
 PI Schulte-Merker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;  
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Björke LM, Hal B;  
 PI Adamkewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;  
 PI Nicoll M;  
 XX WPI; 2004-365506/34.  
 DR N-PSDB; ADS92934.  
 XX  
 PT Identifying a candidate branching morphogenesis modulating agent for  
 PT treating cancer comprises contacting the assay system comprising a MBM  
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-  
 PT biased activity.  
 XX  
 PS Example 3; SEQ ID NO 36; 179pp; English.  
 XX  
 CC The invention describes a method of identifying a candidate branching  
 CC morphogenesis modulating (MBM) agent. The method comprises: providing an  
 CC assay system comprising a MBM polypeptide or nucleic acid; contacting the  
 CC assay system with a test agent under conditions where the system provides  
 CC a reference activity, except for the presence of the test agent; and  
 CC detecting a test agent-biased activity of the assay system, where a  
 CC difference between the test agent-biased activity and the reference  
 CC activity identifies the test agent as a candidate branching morphogenesis  
 CC modulating agent. Also described are: a method of modulating branching  
 CC morphogenesis in a mammalian cell; and a method for diagnosing a disease  
 CC in a patient. The method is useful in identifying a candidate branching  
 CC morphogenesis modulating agent for preparing a composition for diagnosing  
 CC or treating cancer. This is the amino acid sequence of a human branching  
 CC morphogenesis modulating (MBM) protein.  
 XX  
 SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 5e-210;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPTTSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQDPDRPQEVSYDTDK 70  
 DB 1 MSGRPTTSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQDPDRPQEVSYDTDK 60  
 QY 71 VTGNGSFGVYQAKLCSGELVAIKVQLQDKRPNRLEQIMRKLDHCNIVRLRYFFYSYG 130  
 DB 61 VTGNGSFGVYQAKLCSGELVAIKVQLQDKRPNRLEQIMRKLDHCNIVRLRYFFYSYG 120  
 QY 131 EKKDEVYANLVLDYVPETVYRVARHYHSAKQTLPTVYVVKLYMYQLFRSLAYIHSFGICHR 190  
 DB 121 EKKDEVYANLVLDYVPETVYRVARHYHSAKQTLPTVYVVKLYMYQLFRSLAYIHSFGICHR 180  
 QY 191 DIKPNQLLLDPTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPERLIFGATDYSIDV 250  
 DB 181 DIKPNQLLLDPTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPERLIFGATDYSIDV 240  
 QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIRREMNPNTYEFKFPQIKAH 310  
 DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIRREMNPNTYEFKFPQIKAH 300  
 QY 311 WTKVFRPTTPEAIALCSRLLEYTPARTLTPLECAHSPFDELDRDNNVHPNGRDTPALF 370  
 DB 301 WTKVFRPTTPEAIALCSRLLEYTPARTLTPLECAHSPFDELDRDNNVHPNGRDTPALF 360  
 QY 371 NFFTQELSSNPPLATILIPPHARI 394  
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 9  
 ADT92555  
 ID ADT92555 standard; protein; 420 AA.  
 XX AC ADT92555;  
 XX 13-JAN-2005 (first entry)  
 DT Human glycogen synthase kinase-3-related protein - SEQ ID 1.  
 XX  
 DE  
 XX neuroregenerative drug; glycogen synthase kinase-3; GSK-3;  
 KW neurological disease; Parkinson's disease; Alzheimer's disease;  
 KW Down's syndrome; cerebrovascular accident; stroke; spinal injury;  
 KW Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;  
 KW epilepsy; anxiety disorder; schizophrenia; depression;  
 KW manic-depressive psychosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004091663-A1.  
 XX 28-OCT-2004.  
 PD  
 XX 16-APR-2004; 2004WO-JP005503.  
 PF  
 XX 18-APR-2003; 2003JP-00114579.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Morishita T, Sakurada K, Suzuki K, Ikeda S;  
 PI WPI; 2004-784511/77.  
 DR N-PSDB; ADT92556.  
 DR  
 XX Neuroregenerative drug for treating neurological disease e.g. Parkinson's  
 PT disease, Alzheimer's disease and Down's syndrome, contains substance  
 PT which inhibits activity of glycogen synthase kinase-3 as active  
 PT ingredient.  
 PT  
 XX Disclosure; SEQ ID NO 1; 115pp; Japanese.  
 PS  
 XX The invention comprises a neuroregenerative drug that inhibits the  
 CC activity of glycogen synthase kinase-3 (GSK-3). The neuroregenerative  
 CC drug of the invention is useful for treating neurological disease, such  
 CC as: Parkinson's disease, Alzheimer's disease, Down's syndrome,  
 CC

CC cerebrovascular accident, stroke, spinal injury, Huntington's chorea,  
 CC multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety  
 CC disorder, schizophrenia, depression and manic-depressive psychosis. The  
 CC present human protein is used in the exemplification of the invention.  
 XX  
 SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 5e-210;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 70  
 Db 1 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 60

Qy 71 VINGSGVGVYQAKLDCSGELVAIKVLDKRFKRNRELIQMRKLDHCNIVRLRYFFSSG 130  
 Db 61 VINGSGVGVYQAKLDCSGELVAIKVLDKRFKRNRELIQMRKLDHCNIVRLRYFFSSG 120

Qy 131 EKDEVLNLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 190  
 Db 121 EKDEVLNLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 180

Qy 191 DIKPNLLDPDPTAVLKCDFGSAKQVRCGPVNSYICSRYYRAPELIFGATDYSIDV 250  
 Db 181 DIKPNLLDPDPTAVLKCDFGSAKQVRCGPVNSYICSRYYRAPELIFGATDYSIDV 240

Qy 251 WSAGCVLAELLGQPIPPGDSGVQDQVEIIVKVLGTPTRREQIREMNPNTYEFKFPQIKAH 310  
 Db 241 WSAGCVLAELLGQPIPPGDSGVQDQVEIIVKVLGTPTRREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTPEALCSRLLEYTPPTARLTPLECAHSAHFFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPTPEALCSRLLEYTPPTARLTPLECAHSAHFFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 10  
 ADR06333  
 ID ADR06333 standard; protein; 414 AA.  
 XX  
 AC ADR06333;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE p38-alpha kinase, SEQ ID 31.  
 XX  
 KW Switch control ligand; switch control pocket;  
 KW protein activity modulation; human; p38-alpha kinase; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004061084-A2.  
 XX  
 PD 22-JUL-2004.  
 XX  
 PF 26-DEC-2003; 2003WO-US041450.  
 XX  
 PR 31-DEC-2002; 2002US-0437304P.  
 PR 31-DEC-2002; 2002US-0437403P.  
 PR 31-DEC-2002; 2002US-0437415P.  
 PR 31-DEC-2002; 2002US-0437487P.  
 PR 18-APR-2003; 2003US-0463804P.  
 PR 24-DEC-2003; 53US-00463804.  
 XX  
 PA (DECI-) DECIPHERA PHARM INC.  
 XX  
 PI Flynn DL, Petrillo PA;  
 XX  
 XX WPI; 2004-534376/51.  
 DR

XX Identifying molecules that interact with specific naturally occurring  
 PT proteins for modulating protein activity, comprises identifying molecules  
 PT that bind with the protein at the region of the pocket to regulate  
 PT activity of the protein.  
 XX  
 PS Disclosure; SEQ ID NO 31; 204pp; English.  
 XX  
 CC The present invention relates to a method for identifying molecules,  
 CC which interact with proteins e.g. enzymes, receptors, or signaling  
 CC proteins, in order to regulate the activity of the proteins. The method  
 CC comprises: identifying a switch control ligand forming a part of the  
 CC protein; identifying a switch control pocket forming a part of the  
 CC protein and which interacts with the switch control ligand, where the  
 CC ligand interacting in vivo with the pocket to regulate the conformation  
 CC and biological activity of the protein so that the protein will assume a  
 CC first conformation and a first biological activity upon the ligand-pocket  
 CC interaction, and will assume a second, different conformation and a  
 CC biological activity in the absence of the ligand-pocket interaction;  
 CC providing respective samples of the protein in the first and second  
 CC conformations; and screening at least one of the samples against one or  
 CC more candidate molecules by contacting the molecules and one sample, and  
 CC identifying small molecules which bind with the protein at the region of  
 CC the pocket in order to regulate the activity of the protein. The method  
 CC is useful for modulating protein activity and for the identification of  
 CC new pharmacological compounds and for treatment modalities. The present  
 CC sequence is p38-alpha kinase for which a switch control ligand was  
 CC produced.  
 XX  
 SQ Sequence 414 AA;

Query Match 96.7%; Score 2013; DB 8; Length 414;  
 Best Local Similarity 99.7%; Pred. No. 7.6e-209;  
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 70  
 Db 1 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 60

Qy 71 VINGSGVGVYQAKLDCSGELVAIKVLDKRFKRNRELIQMRKLDHCNIVRLRYFFSSG 130  
 Db 61 VINGSGVGVYQAKLDCSGELVAIKVLDKRFKRNRELIQMRKLDHCNIVRLRYFFSSG 120

Qy 131 EKDEVLNLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 190  
 Db 121 EKDEVLNLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 180

Qy 191 DIKPNLLDPDPTAVLKCDFGSAKQVRCGPVNSYICSRYYRAPELIFGATDYSIDV 250  
 Db 181 DIKPNLLDPDPTAVLKCDFGSAKQVRCGPVNSYICSRYYRAPELIFGATDYSIDV 240

Qy 251 WSAGCVLAELLGQPIPPGDSGVQDQVEIIVKVLGTPTRREQIREMNPNTYEFKFPQIKAH 310  
 Db 241 WSAGCVLAELLGQPIPPGDSGVQDQVEIIVKVLGTPTRREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTPEALCSRLLEYTPPTARLTPLECAHSAHFFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPTPEALCSRLLEYTPPTARLTPLECAHSAHFFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 11  
 AAR61327  
 ID AAR61327 standard; protein; 420 AA.  
 XX  
 AC AAR61327;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 21-APR-1995 (first entry)  
 XX

```
DE Tau-protein kinase I (TPK-I), Alzheimer's disease.
XX
XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease.
XX
OS Rattus rattus.
XX
XX EP616032-A2.
XX
XX 21-SEP-1994.
XX
XX 01-MAR-1994; 94EP-00103057.
XX
XX 02-MAR-1993; 93JP-00041160.
XX
XX 22-MAR-1993; 93JP-00085143.
XX
XX 02-AUG-1993; 93JP-00191246.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX
XX (MITU ) MITSUBISHI CHEM CORP.
XX
XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A,
XX
XX Sato S;
XX
XX WPI; 1994-287181/36.
XX
XX N-PSDB; AAQ67459.
XX
XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-
XX
XX protein providing means for prevention and treatment of Alzheimer's
XX
XX disease.
XX
XX Claim 4; Page 18; 30pp; English.
XX
XX AAQ67459 codes for a newly isolated tau-protein kinase I enzyme (TPK-1),
XX
XX shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a
XX
XX rat fetus brain cDNA library, and was expressed in insect cells. TPK-I
XX
XX acts specifically on tau-protein, which is thought to be involved in
XX
XX Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped
XX
XX that the characterisation of TPK-I may lead to development of new agents
XX
XX for the prevention and therapy of these diseases. (Updated on 25-MAR-2003
XX
XX to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 420 AA;
XX
XX Query Match 96.7%; Score 2013; DB 2; Length 420;
XX
XX Best Local Similarity 99.7%; Pred. No. 7.8e-209;
XX
XX Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 11 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSVDKSGKVTTVVATPGQDPDPQEVSYDTDK 70
XX
XX 1 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSVDKSGKVTTVVATPGQDPDPQEVSYDTDK 60
XX
XX 71 VINGSGGVVYQAKLDSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 130
XX
XX 61 VINGSGGVVYQAKLDSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 120
XX
XX 131 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFSLAYIHSGFCHR 190
XX
XX 121 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFSLAYIHSGFCHR 180
XX
XX 191 DIKQNLDDPDPTAVLKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 250
XX
XX 181 DIKQNLDDPDPTAVLKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 240
XX
XX 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPTRREQIRENNPNYTFKFPQIAHP 310
XX
XX 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPTRREQIRENNPNYTFKFPQIAHP 300
XX
XX 311 WTKVFRPTTPEALACSLLEVTPTARLTLEACAHSPFDELDPNVKHPNGRDTPALF 370
XX
XX 301 WTKVFRPTTPEALACSLRLLEYTPTARLTLEACAHSPFDELDPNVKHPNGRDTPALF 360
XX
XX 371 NFFTQELSSNPPLATILIPPHARI 394
XX
XX 361 NFFTQELSSNPPLATILIPPHARI 384
XX
XX RESULT 12
XX
XX ABB77875 standard; peptide; 420 AA.
XX
XX AC ABB77875;
XX
XX 27-SEP-2002 (first entry)
XX
XX Amino acid sequence of glycogen synthase kinase 3 isoform beta.
XX
XX Glycogen synthase kinase 3 beta; GSK3beta; T-cell lymphoma; stroke;
XX
XX Type II diabetes mellitus; obesity; neurodegenerative disorder; cancer;
XX
XX Alzheimer's disease; mood disorder; depression; schizophrenia;
XX
XX cyclin-dependent kinase 2; substrate; protein coordinate data.
XX
XX OS Homo sapiens.
XX
XX WO20020254-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-GB005632.
XX
XX 18-DEC-2000; 2000GB-00030846.
XX
XX 14-AUG-2001; 2001GB-00019796.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Bax B, Brown M, Reith A;
XX
XX WPI; 2002-519885/55.
XX
XX Novel crystal structures comprising glycogen synthase kinase (GSK)-3 beta
XX
XX protein or crystal structure comprising a GSK-3 beta: frequently
XX
XX rearranged in advanced T-cell lymphomas (PRAT)-tide complex in
XX
XX crystalline form.
XX
XX Claim 6; Page 23; 327pp; English.
XX
XX The specification describes the structure of glycogen synthase kinase
XX
XX (GSK)3beta protein in crystalline form. GSK3beta is frequently rearranged
XX
XX in advanced T-cell lymphomas. The crystalline structure of GSK3beta is
XX
XX useful in the design or selection of potential inhibitors and/or
XX
XX activators of GSK3beta kinase activity. Such inhibitors and activators
XX
XX are useful for treating Type II diabetes mellitus, obesity,
XX
XX neurodegenerative disorders such as Alzheimer's disease, stroke and mood
XX
XX disorders such as bipolar and unipolar depression, schizophrenia, cancer,
XX
XX in humans. Because GSK3beta may crystallize in more than one crystal
XX
XX form, the structure coordinates of GSK3 or its portions are particularly
XX
XX useful to solve the structure of other crystal forms of GSK3. They may
XX
XX also be used to solve the structure of GSK3 mutants, GSK3 co-complexes,
XX
XX or of the crystalline form of any other protein, particularly kinases
XX
XX with significant amino acid sequence homology to any functional domain of
XX
XX GSK3. The present sequence represents the beta isoform of GSK3, GSK3beta
XX
XX SQ Sequence 420 AA;
XX
XX Query Match 96.7%; Score 2013; DB 5; Length 420;
XX
XX Best Local Similarity 99.7%; Pred. No. 7.8e-209;
XX
XX Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 11 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSVDKSGKVTTVVATPGQDPDPQEVSYDTDK 70
XX
XX 1 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSVDKSGKVTTVVATPGQDPDPQEVSYDTDK 60
XX
XX 71 VINGSGGVVYQAKLDSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 130
XX
XX 61 VINGSGGVVYQAKLDSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 120
XX
XX 131 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFSLAYIHSGFCHR 190
XX
XX 121 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFSLAYIHSGFCHR 180
XX
XX 191 DIKQNLDDPDPTAVLKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 250
XX
XX 181 DIKQNLDDPDPTAVLKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 240
XX
XX 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPTRREQIRENNPNYTFKFPQIAHP 310
XX
XX 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPTRREQIRENNPNYTFKFPQIAHP 300
XX
XX 311 WTKVFRPTTPEALACSLLEVTPTARLTLEACAHSPFDELDPNVKHPNGRDTPALF 370
XX
XX 301 WTKVFRPTTPEALACSLRLLEYTPTARLTLEACAHSPFDELDPNVKHPNGRDTPALF 360
XX
XX 371 NFFTQELSSNPPLATILIPPHARI 394
XX
XX 361 NFFTQELSSNPPLATILIPPHARI 384
```

Db 121 EKKDEVYLVLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 180  
 Qy 191 DIKPNQLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250  
 Db 181 DIKPNQLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240  
 Qy 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPPREQIREMNPNTYEFKFPQIKAH 310  
 Db 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPPREQIREMNPNTYEFKFPQIKAH 300  
 Qy 311 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGSDTTPALF 370  
 Db 301 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGSDTTPALF 360  
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 13  
 ID ABR44293 standard; protein; 420 AA.  
 XX AC ABR44293;  
 XX DT 22-APR-2003 (first entry)  
 XX DE Human glycogen synthase kinase-3 beta.  
 XX KW Human; enzyme; glycogen synthase kinase-3 beta; protein co-ordinate data;  
 KW neurotropic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;  
 KW antiinflammatory; cardiovascular; antiallergic; antiasthmatic;  
 KW antiparkinsonian; anticonvulsant; dermatological; vasotrophic; GSK-3;  
 KW schizophrenia; Alzheimer's disease; diabetes; autoimmune disease;  
 KW inflammatory disease; metabolic; neurological; neurodegenerative;  
 KW cardiovascular disease; allergy; asthma; Huntington's disease;  
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;  
 KW amyotrophic lateral sclerosis; multiple sclerosis; kinase;  
 KW cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.  
 XX OS Homo sapiens.  
 XX PN WO200288078-A2.  
 XX PD 07-NOV-2002.  
 XX PF 29-APR-2002; 2002WO-US013511.  
 XX PR 30-APR-2001; 2001US-0287366P.  
 XX PR 08-JUN-2001; 2001US-0297094P.  
 XX PR 27-FEB-2002; 2002US-0361899P.  
 XX PA (VERT-) VERTEX PHARM INC.  
 XX PI Ter Haar E, Swenson L, Green J, Arnost MJ;  
 XX WPI; 2003-247844/24.  
 XX PT New pyrazolo(3,4-c)pyridazine derivatives are glucagon synthase kinase-3  
 PT inhibitors useful for treating e.g. schizophrenia, Alzheimer's disease, and  
 PT diabetes, autoimmune diseases, allergy, asthma, multiple sclerosis, and  
 PT baldness.  
 XX PS Claim 36; Page 777-778; 778pp; English.  
 XX CC The present invention relates to novel pyrazolo(3,4-c)pyridazine  
 CC derivatives, which have glucagon synthase kinase-3 (GSK-3) inhibitory  
 CC activity. The derivatives are useful for inhibiting beta-catenin  
 CC phosphorylation and hyperphosphorylated Tau protein production in a  
 CC patient and GSK-3 activity in a patient or in a biological sample. The  
 CC derivatives are also useful for treating schizophrenia, Alzheimer's  
 CC disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,  
 CC neurological and neurodegenerative diseases, cardiovascular diseases,

CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related  
 CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple  
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.  
 CC The present sequence is human GSK-3 beta, used to illustrate the  
 CC invention. GSK-3 beta is a serine/threonine protein kinase  
 XX Sequence 420 AA;  
 SQ Query Match 96.7%; Score 2013; DB 6; Length 420;  
 Best Local Similarity 99.7%; Pred. No. 7.8e-209;  
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 11 MSGRPRTTSAEACKPVQPSAFSGSMKVS RDGSKVTVTVVATGQGPDRPQEVSYTDTK 70  
 Db 1 MSGRPRTTSAEACKPVQPSAFSGSMKVS RDGSKVTVTVVATGQGPDRPQEVSYTDTK 60  
 Qy 71 VIGNSGFVVYQAKLCDSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 130  
 Db 61 VIGNSGFVVYQAKLCDSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 120  
 Qy 131 EKKDEVYLVLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 190  
 Db 121 EKKDEVYLVLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 180  
 Qy 191 DIKPNQLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250  
 Db 181 DIKPNQLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240  
 Qy 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPPREQIREMNPNTYEFKFPQIKAH 310  
 Db 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIIVKVLGTPPREQIREMNPNTYEFKFPQIKAH 300  
 Qy 311 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGSDTTPALF 370  
 Db 301 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGSDTTPALF 360  
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394  
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 14  
 ABR44293  
 ID ABR44293 standard; protein; 420 AA.  
 XX AC ABR44293;  
 XX DT 18-AUG-2003 (first entry)  
 XX DE Human glycogen synthase kinase-3 (GSK3)beta polypeptide.  
 XX KW GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;  
 KW vulnary; antiarteriosclerotic; GSK3beta; enzyme.  
 XX OS Homo sapiens.  
 XX PN WO2003038037-A2.  
 XX PD 08-MAY-2003.  
 XX PF 23-OCT-2002; 2002WO-US033909.  
 XX PR 29-OCT-2001; 2001US-0350160P.  
 XX PR 13-NOV-2001; 2001US-0337905P.  
 XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.  
 XX PI Walsh K;  
 XX WPI; 2003-482140/45.  
 XX PT Modulating angiogenesis, useful for treating hyperlipidemia, comprises  
 PT administering an angiogenesis inhibitor/promoter, such as an



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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:07:20 ; Search time 40 Seconds  
(without alignments)  
947.735 Million cell updates/sec

Title: US-10-733-816-2  
Perfect score: 2081  
Sequence: 1 MEYMPMEGGMGSRPRTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	97.3	420	1 S53324	glycogen synthase
2	2010	96.6	420	1 TVRTEB	tau-protein kinase
3	1931	92.8	420	2 I51425	intracellular kina
4	1923	92.4	420	2 I51425	glycogen synthase
5	1607	77.2	483	1 TVRTEA	protein kinase (EC
6	1590.5	76.4	575	2 S35327	protein kinase egg
7	1542.5	74.1	733	2 S10932	probable protein k
8	1542.5	74.1	1067	2 S35423	protein kinase egg
9	1342.5	64.5	362	2 T26520	hypothetical prote
10	1296	62.3	409	2 S51105	shaggy protein kin
11	1275.5	61.3	471	2 T03601	shaggy protein kin
12	1273.5	61.2	471	1 T02297	shaggy protein kin
13	1265	60.8	408	2 T48637	protein kinase MSK
14	1258	60.5	472	1 T01236	serine/threonine-s
15	1256	60.4	412	1 S37642	protein kinase MSK
16	1249	60.0	403	2 T03777	probable shaggy-li
17	1249	60.0	431	2 S51106	shaggy protein kin
18	1247.5	59.9	469	1 T02256	shaggy protein kin
19	1246	59.9	409	1 S41597	protein kinase ASK
20	1245	59.8	412	2 S71266	shaggy-like protei
21	1244	59.8	411	1 S37643	protein kinase MSK
22	1239	59.5	409	2 S52095	tau-protein kinase
23	1234	59.3	380	2 T04863	shaggy-like protei
24	1233	59.3	412	2 A84715	probable shaggy-li
25	1232	59.2	405	1 S41596	protein kinase ASK
26	1232	59.2	407	2 S77922	shaggy-like protei
27	1229.5	59.1	420	2 A96613	probable glycogen
28	1229.5	59.1	469	1 T02254	shaggy protein kin
29	1228.5	59.0	447	2 F86232	hypothetical prote

protein kinase MSK  
shaggy-like protei  
protein kinase Atk  
hypothetical prote  
protein kinase (EC  
shaggy-like kinase  
protein kinase skp  
protein kinase skp  
serine-threonine p  
probable protein k  
glycogen synthase  
hypothetical prote  
protein kinase RIM  
MKK1 protein - yea  
probable serine/th  
hypothetical prote

30 1226 58.9 411 1 S37644  
31 1226 58.9 468 2 T08139  
32 1220 58.6 421 2 S51938  
33 1208 58.0 447 2 T01756  
34 1178 56.6 468 2 A55476  
35 1158 55.6 431 2 T47908  
36 1156.5 55.6 387 2 T37758  
37 1109.5 53.3 354 2 T45138  
38 996 47.9 381 2 T40746  
39 996 47.9 390 2 T43008  
40 978.5 47.0 452 2 T18457  
41 940.5 45.2 354 2 F90121  
42 940 45.2 370 2 A56347  
43 873.5 42.0 501 2 S67615  
44 792 38.1 211 2 T04119  
45 735.5 35.3 367 2 T19937

ALIGNMENTS

glycogen synthase kinase 3 beta (EC 2.7.1.1) - human  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S53324  
R;Stambolic, V.; Woodgett, J.R.  
Biochem. J. 303, 701-704, 1994  
A;Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via ser  
A;Reference number: S53324; MUID:95071278; PMID:7980435  
A;Accession: S53324  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-420 <STA>  
A;Cross-references: UNIPROT:P49841; UNIPARC:UPI000004E93D; EMBL:L33801; NID:9529236; PID:  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
C;Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (see  
C;Genetics:  
A;Gene: GDB:GSK3B  
A;Cross-references: GDB:6108057  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphoprotein; phosphotransferase  
F;54-315/Domain: protein kinase homology <KIN>  
F;62-70/Region: protein kinase ATP-binding motif  
F;9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status ex  
F;85/Active site: Lys #status predicted

Query Match 97.3%; Score 2024; DB 1; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.6e-89;  
Matches 384; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSVDKGSKVTTVVATPGQPDPRPOEVSYYDTK 70  
Db 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSVDKGSKVTTVVATPGQPDPRPOEVSYYDTK 60  
Qy 71 VIGNSGFVVYQAKLDCSGLVAKKVLQDKRFKRELQIMRKLDHNCNIVLRYFFVSSG 130  
Db 61 VIGNSGFVVYQAKLDCSGLVAKKVLQDKRFKRELQIMRKLDHNCNIVLRYFFVSSG 120  
Qy 131 EKDEVTNLVLDVYPETVYVARHYHSAKQTLPIVYVKLYMYQLFSLAYIHSFGICHR 190  
Db 121 EKDEVTNLVLDVYPETVYVARHYHSAKQTLPIVYVKLYMYQLFSLAYIHSFGICHR 180  
Qy 191 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDTSIDV 250  
Db 181 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDTSIDV 240  
Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPFREQIREMNPNTYEFKFPQIAHP 310  
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPFREQIREMNPNTYEFKFPQIAHP 300  
Qy 311 WTKVFRPRTPEALCSRLLETTYPTARLTIPLECAHSAFDELDPNVKHPNGRDTALF 370

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Db 301 WTKVFRPTTPEAALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 2
TVRTKB
tau-protein kinase (EC 2.7.1.135) I - rat
N;Alternate names: factor A: Glycogen synthase kinase 3 beta; protein kinase GSK-3-beta;
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S14708; S33741; S36729
R;Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A;Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A;Reference number: S14707; MUID:90316097; PMID:2164470
A;Molecule type: mRNA
A;Accession: S14708
A;Residues: 1-420 <MOO>
A;Cross-references: UNIPROT:P18266; UNIPARC:UPI000012DDC0; EMBL:X53428; NID:G56333; PIDN:
A;Note: the author translated the codon ATG for residue 240 as Val
R;Ishiguro, K.; Shiratsuchi, A.; Sato, S.; Omori, A.; Arioka, M.; Kobayashi, S.; Uchida,
FEBS Lett. 325, 167-172, 1993
A;Title: Glycogen synthase kinase 3-beta is identical to tau protein kinase I generating
A;Reference number: S33741; MUID:93307488; PMID:7686508
A;Accession: S33741
A;Molecule type: mRNA
A;Residues: 1-239, 'V', 241-420 <ISH>
A;Cross-references: UNIPARC:UPI00000018B4; EMBL:X73653; NID:G402651; PIDN:CAA52020.1; PIDN:
A;Accession: S36729
A;Molecule type: protein
A;Residues: 37-58; 61-74; 151-158; 293-316; 318-325; 327-332; 351-368; 370-375 <ISH2>
A;Cross-references: UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538;
S3D
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;85/Active site: Lys #status predicted

Query Match 36.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240

QY 251 WSAGCVLAELLGQPIFPGDSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPGDSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

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Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
I51425
intracellular kinase (EC 2.7.1.1-) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51425
R;Pierce, S.B.; Kimelman, D.
Development 121, 755-765, 1995
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Reference number: I51425; MUID:95237008; PMID:7720580
A;Accession: I51425
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-420 <PIE>
A;Cross-references: UNIPROT:Q91757; UNIPARC:UPI00000FB682; GB:L38492; NID:G727189; PIDN:
C;Genetics:
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;85/Active site: Lys #status predicted

Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 6.5e-85;
Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPNLLDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240

QY 251 WSAGCVLAELLGQPIFPGDSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPGDSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 393
Db 361 NFFTQELSSNPPLATILIPPHARI 383

RESULT 4
I51692
glycogen synthase kinase (EC 2.7.1.1-) 3 beta - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51692
R;Dominguez, I.; Itoh, K.; Sokol, S.Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 8498-8502, 1995
A;Title: Role of glycogen synthase kinase 3 beta as a negative regulator of dorsoventral
A;Reference number: I51692; MUID:95396823; PMID:7667318
A;Accession: I51692
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-420 <DOM>

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A;Cross-references: UNIPROT:Q91627; UNIPARC:UPI000000FBE97; EMBL:U31862; NID:gl000734; Pf  
 C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: ATP; phosphotransferase  
 F;54-315/Domain: protein kinase homology <KIN>  
 F;62-70/Region: protein kinase ATP-binding motif  
 F;85/Active site: Lys #status predicted

Query Match 92.4%; Score 1923; DB 2; Length 420;  
 Best Local Similarity 95.0%; Pred. No. 1.6e-89;  
 Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSVDKSGSKVTTVATPGQGPDRPQSVYTDTK 70  
 Db 1 MSGRPRTTSFAESCKPVQPSFGSMKVSVDKSGSKVTTVATPGQGPDRPQSVYTDTK 60  
 Qy 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130  
 Db 61 VINGSGFVVYQAKLDCDTGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120  
 Qy 131 EKDEVLNLVLDVYPTVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFGICHR 190  
 Db 121 EKDEVLNLVLDVYPTVTVARHYSRAKQALPIIYVVKLYMYQLFRSLAYIHSFGICHR 180  
 Qy 191 DIKPNLLDPDTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250  
 Db 181 DIKPNLLDPDTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240  
 Qy 251 WSAGCVLAELLGQPIFFPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 310  
 Db 241 WSAGCVLAELLGQPIFFPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 300  
 Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPELCAHSPFDELDPNVKHPNGRDTPALF 370  
 Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPELCAHSPFDELDPNVKHPNGRDTPALF 360  
 Qy 371 NPTQELSSNPPLATILIPPHAR 393  
 Db 361 NPTQELSSNPPLATILIPPHAR 383

## RESULT 5

TVTKA

protein kinase (EC 2.7.1.37) GSK-3-alpha - rat  
 N;Alternate names: factor A; glycogen synthase kinase 3 alpha  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C;Accession: S14707  
 R;Woodgett, J.R.  
 EMBO J. 9, 2431-2438, 1990  
 A;Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.  
 A;Reference number: S14707; MUID:90316097; PMID:2164470  
 A;Accession: S14707  
 A;Molecule type: mRNA  
 A;Residues: 1-483 <WO>  
 A;Cross-references: UNIPROT:P18265; UNIPARC:UPI000012DDBF; EMBL:X53427; NID:956331; PIDN  
 C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
 F;117-378/Domain: protein kinase homology <KIN>  
 F;125-133/Region: protein kinase ATP-binding motif  
 F;148/Active site: Lys #status predicted

Query Match 77.2%; Score 1607; DB 1; Length 483;  
 Best Local Similarity 80.6%; Pred. No. 1.6e-69;  
 Matches 312; Conservative 23; Mismatches 38; Indels 14; Gaps 3;

Qy 8 GGGMSGRPRT-TSPAESCKPVQPSAFGSMKVSVDKSGSKVTTVATPGQGPDRPQSVY 66  
 Db 73 GGGSGGFGAGTSPFP-----GVKLR--DSGKVTTVATVATLGQGPERSQEVAY 119  
 Qy 67 TDTKVIKNGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFF 126  
 Db 120 TDKIKVINGSGFVVYQALRAETRELVAIKVLDQKRFKNRELQIMRKLDHCNIVRLRYFF 179

Qy 127 YSSEKKKDEVYLVLDVYPTVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFG 186  
 Db 180 YSSEKKKDEVYLVLDVYPTVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFG 239  
 Qy 187 ICHRDIKPQNLLDPDTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTS 246  
 Db 240 VCHRDIKPQNLLDPDTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTS 299  
 Qy 247 SIDWSAGCVLAELLGQPIFFPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQI 306  
 Db 300 SIDWSAGCVLAELLGQPIFFPGSGVDQVLEIKVLGTPTREQIREMNPNTYEFKPKQI 359  
 Qy 307 KAHPTWKVFRPRTPEPAIALCSRLLEYTPPTARLTPELCAHSPFDELDPNVKHPNGRDT 366  
 Db 360 KAHPTWKVFRPRTPEPAIALCSRLLEYTPPTARLTPELCAHSPFDELDPNVKHPNGRDT 419  
 Qy 367 PALFNFTTQELSSNPPLATILIPPHAR 393  
 Db 420 PPLFNFPGLSGLSQPSLNAILIPHLR 446

## RESULT 6

S35327

protein kinase seg39 (EC 2.7.1.1-) (clone pNB39) - fruit fly (Drosophila melanogaster)  
 N;Alternate names: zw3-A  
 C;Contains: protein kinase (EC 2.7.1.37)  
 C;Species: Drosophila melanogaster  
 C;Date: 19-Jul-1996 #sequence\_revision 01-Nov-1996 #text\_change 05-Oct-2004  
 C;Accession: S35327; S35326; S35329; A44331; S11675; S10931; S35421; S35422; S35424  
 R;Ruel, L.; Pantescio, V.; Lutz, Y.; Simpson, P.; Bourouis, M.  
 EMBO J. 12, 1657-1669, 1993

A;Title: Functional significance of a family of protein kinases encoded at the shaggy loc  
 A;Reference number: S35325; MUID:93223707; PMID:8467811  
 A;Accession: S35327

A;Molecule type: mRNA  
 A;Residues: 1-575 <RUE>  
 A;Cross-references: UNIPROT:P18431; UNIPARC:UPI000002B384; EMBL:X70863; NID:g11145; PIDN  
 A;Accession: S35326  
 A;Molecule type: mRNA  
 A;Residues: 1-196, 'R', '198-394', 'D', '396-512', 'D', '514' <RU2>  
 A;Cross-references: UNIPARC:UPI000016BD6A; EMBL:X70862; NID:g11143; PIDN:CAA50212.1; PID  
 A;Accession: S35329  
 A;Molecule type: mRNA  
 A;Residues: 1-42 <RU3>

A;Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CAA50215.1; PID  
 A;Note: the translation of the nucleotide sequence is not complete in this paper  
 R;Siegfried, E.; Chou, T.B.; Perrimon, N.  
 Cell 71, 1167-1179, 1992

A;Title: wingless signaling acts through zeste-white 3, the Drosophila homolog of glycose  
 A;Reference number: A44331; MUID:93113685; PMID:1335365  
 A;Accession: A44331

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar  
 A;Molecule type: mRNA  
 A;Residues: 1-445, 'R', '447-510', 'DVTDTS' <SIE>  
 A;Cross-references: UNIPARC:UPI000017A460  
 R;Bourouis, M.; Moore, P.; Ruel, L.; Grau, Y.; Heitzler, P.; Simpson, P.  
 EMBO J. 9, 2877-2884, 1990  
 A;Title: An early embryonic product of the gene shaggy encodes a serine/threonine protease  
 A;Reference number: S11675; MUID:90361000; PMID:2118107  
 A;Accession: S11675

A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-243, 'I', '245-405', 'A', '407-512', 'D', '514' <BOU>  
 A;Cross-references: UNIPARC:UPI000016BD69; EMBL:X53332; NID:g10895; PIDN:CAA37419.1; PID  
 R;Siegfried, E.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.  
 Nature 345, 825-829, 1990

A;Title: Putative protein kinase product of the Drosophila segment-polarity gene zeste-w  
 A;Reference number: S10931; MUID:90294930; PMID:2113617  
 A;Accession: S10931  
 A;Molecule type: mRNA  
 A;Residues: 1-289 <S12>

A;Cross-references: UNIPARC:UPI000016BE19; EMBL:X54005; NID:c8859; PIDN:CAA37951.1; PID:c  
 A;Experimental source: ovarian cdna library

C;Genetics:  
A;Gene: FlyBase:sgg  
A;Cross-references: FlyBase:FBgn0003371  
C;Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threonine kinase; protein kinase ATP-binding motif  
F;52-313/Domain: protein kinase homology <KIN>  
F;60-68/Region: protein kinase ATP-binding motif

Query Match 76.4%; Score 1590.5; DB 2; Length 575;  
Best Local Similarity 79.6%; Pred. No. 1.1e-68;  
Matches 305; Conservative 32; Mismatches 41; Indels 5; Gaps 4;

QY 11 MSGRPRRTTSFAESC---KPVQPS-AFGSMKVSRLDGGKVTIVVATPGQDPDRPQSVSTDT 69  
DB 1 MSGRPRRTSSFAENK--QSPSLVGGVTC-SRDGSKITTVVATPGQDTRDQGEVSTDT 57

QY 70 KVIINGSFGVYQAKLDCSDGELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRLRYFFYS 129  
DB 58 KVIINGSFGVVFQAKLDCDGTGELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRLRYFFYS 117

QY 130 GEKKDEVILNLVDYVPETVYRVARHYSRAKOTLPVIVYKLYMYQLFRSLAYIHSFGICH 189  
DB 118 GEKKDEVILNLVLEIYPTVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYIHSFGICH 177

QY 190 RDIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYSID 249  
DB 178 RDIKPQNLLDPTAVLKLCDFGSAKOLHGEPNVSYICSRYYRAPELIFGAINYTKID 237

QY 250 VMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFKPPQIKAH 309  
DB 238 VMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFKPPQIKSH 297

QY 310 PWTQVPRPPTPEAIALCSRLLEYTPARLTPLLEACAHSPFDELRLDPNVKHPNGRDTPA 368  
DB 298 PWQKHPQKVRIPRTPTPEAINLVSLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLP 357

QY 369 LNFTTQELSSNPPLATILIPPH 391  
DB 358 LNFTTEHLSIQPSLVPLPKH 380

RESULT 7  
S10932  
probable protein kinase zeste-white3 (EC 2.7.1.1-) (clone cK25) - fruit-fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 05-Oct-2004  
C;Accession: S10932  
R;Siegfried, B.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.  
Nature 345, 825-829, 1990  
A;Title: Putative protein kinase product of the Drosophila segment-polarity gene zeste-white3  
A;Reference number: S10931; MUID: 90294930; PMID: 2113617  
A;Accession: S10932  
A;Molecule type: mRNA  
A;Residues: 1-733 <SITE>  
A;Cross-references: UNIPARC:UPI00016BE18; EMBL:X54006; NID:98857; PIDN:CAA37952.1; PID: S10932  
A;Experimental source: embryonic CDNA library  
A;Note: it is uncertain whether Met-1 or Met-44 is the initiator or whether translation starts at Met-1  
C;Genetics:  
A;Gene: zw3  
A;Cross-references: FlyBase:FBgn0003371  
C;Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threonine kinase; protein kinase homology <KIN>  
F;285-546/Domain: protein kinase homology <KIN>  
F;293-301/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 733;  
Best Local Similarity 75.9%; Pred. No. 2.5e-66;  
Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

QY 7 EGGMSGRPRRTTSFAESC---KPVQPSAFGSMKVSRLDGGKVTIVVATPGQDPDRPQ 62  
DB 230 DSGGENVKTAKLARTQSCVSWTKVQK-----FKNILGRDGSKITTVVATPGQDTRVQ 283

QY 63 EVSYTDTKVIINGSFGVYQAKLDCSDGELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRL 122  
DB 63 EVSYTDTKVIINGSFGVYQAKLDCDGTGELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 122

DB 284 EVSYTDTKVIINGSFGVYQAKLDCDGTGELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 343  
QY 123 RYFFYSSGKKDEVILNLVDYVPETVYRVARHYSRAKOTLPVIVYKLYMYQLFRSLAYI 182  
DB 344 LYFFYSSGKKDEVILNLVLEIYPTVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYI 403

QY 183 HSPGICHRODIKPNLLDPTAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFGAT 242  
DB 404 HSLGICHRODIKPNLLDPTAVLKLCDFGSAKOLHGEPNVSYICSRYYRAPELIFGAI 463

QY 243 DYTSSIDVMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFK 302  
DB 464 NYTKIDVMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFK 523

QY 303 FPOIKAHPTKVRPPTPEAIALCSRLLEYTPARLTPLLEACAHSPFDELRLDPNVKHP 361  
DB 524 FPOIKSHPMQKVRIPRTPTPEAINLVSLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLP 583

QY 362 NGRDTEPALNFTTQELSSNPPLATILIPPH 391  
DB 584 NGRDMPPLNFTTEHLSIQPSLVPLPKH 613

RESULT 8  
S35423  
protein kinase egg46 (EC 2.7.1.1-) - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004  
C;Accession: S35423  
R;Ruel, L.; Pantescio, V.; Lutz, Y.; Simpson, P.; Bourouf, M.  
EMBO J. 12, 1657-1669, 1993  
A;Title: Functional significance of a family of protein kinases encoded at the shaggy locus  
A;Reference number: S35325; MUID: 93223707; PMID: 8467811  
A;Accession: S35328  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1067 <SUB>  
A;Cross-references: UNIPARC:UPI000013591B; EMBL:X70864; NID:gl1147; PIDN:CAA50214.1; PID: S35423  
C;Genetics:  
A;Gene: FlyBase:sgg  
A;Cross-references: FlyBase:FBgn0003371  
C;Keywords: ATP; phosphotransferase  
F;605-866/Domain: protein kinase homology <KIN>  
F;613-621/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 1067;  
Best Local Similarity 75.9%; Pred. No. 3.5e-66;  
Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

QY 7 EGGMSGRPRRTTSFAESC---KPVQPSAFGSMKVSRLDGGKVTIVVATPGQDPDRPQ 62  
DB 550 DSGGENVKTAKLARTQSCVSWTKVQK-----FKNILGRDGSKITTVVATPGQDTRVQ 603

QY 63 EVSYTDTKVIINGSFGVYQAKLDCSDGELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRL 122  
DB 604 EVSYTDTKVIINGSFGVYQAKLDCDGTGELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 663

QY 123 RYFFYSSGKKDEVILNLVDYVPETVYRVARHYSRAKOTLPVIVYKLYMYQLFRSLAYI 182  
DB 664 LYFFYSSGKKDEVILNLVLEIYPTVYKVARQYAKTKQTIPINFIRLYMYQLFRSLAYI 723

QY 183 HSPGICHRODIKPNLLDPTAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFGAT 242  
DB 724 HSLGICHRODIKPNLLDPTAVLKLCDFGSAKOLHGEPNVSYICSRYYRAPELIFGAI 783

QY 243 DYTSSIDVMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFK 302  
DB 784 NYTKIDVMSAGCVLAELLGQPIFGDSDGVDLVEIKVLGTPTRQIREMNPNTYEFK 843

QY 303 FPOIKAHPTKVRPPTPEAIALCSRLLEYTPARLTPLLEACAHSPFDELRLDPNVKHP 361  
DB 844 FPOIKSHPMQKVRIPRTPTPEAINLVSLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLP 903

Qy 362 NGRDTPALFNTTQELSSNPPLATILPPH 391  
 ||||| ||||| ||||| ||||| |||||  
 Db 904 NGRDMPPLFNTTEHLSIQSLVPLPKH 933  
 ||||| ||||| ||||| ||||| |||||

## RESULT 9

T26520  
 hypothetical protein Y18D10A.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T26520

R;Harris, B.  
 submitted to the EMBL Data Library, December 1998

A;Reference number: Z20226

A;Accession: T26520

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-362 <WLL>

A;Cross-references: UNIPROT:Q9U2Q9; UNIPARC:UPI000007BD45; EMBL:AL034393; PIDN:CAA22311.

A;Experimental source: clone Y18D10A

C;Genetics:

A;Gene: CBSP:Y18D10A.5

A;Introns: 31/3; 121/2; 313/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 64.5%; Score 1342.5; DB 2; Length 362;  
 Best Local Similarity 77.2%; Pred. No. 4e-57;  
 Matches 254; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

Qy 42 KDSKVTTVATPG-QQPDPPQEVSYTDTKVINGSGVYQAKLDCSGELVAIKVQLD 100  
 ||||| ||||| ||||| ||||| |||||

Db 11 KSGKQVTMVASVATDGDVQDQVEISYDQKVIKNGSGVFLAKLSTNEMVAIKVQLD 70  
 ||||| ||||| ||||| ||||| |||||

Qy 101 KRFKNRELQIMRKLDHNCNIVRLRYFFYSSEKDEVLNLDVVPETVYRVARHYSRAK 160  
 ||||| ||||| ||||| ||||| |||||

Db 71 KRFKNRELQIMRKLDHNCNIVRLRYFFYSSEKDEVLNLDVVPETVYRVARHYSKOR 130  
 ||||| ||||| ||||| ||||| |||||

Qy 161 QTLFVIVYKLYMYQLFRSLAYIHSFGICHRDIKPNQLLLDPTAVLKLCDFGSAKQLVRG 220  
 ||||| ||||| ||||| ||||| |||||

Db 131 QQIPMIYVYKLYMYQLFRSLAYIHSFGICHRDIKPNQLLLDPTAVLKLCDFGSAKQLVRN 190  
 ||||| ||||| ||||| ||||| |||||

Qy 221 EPNVSYICSYRYRAPELIFGATDTSIDVWSAGCVLAELLLGQIPFGSGVDQLVEII 280  
 ||||| ||||| ||||| ||||| |||||

Db 191 EPNVSYICSYRYRAPELIFGATDTSIDVWSAGCVLAELLLGQIPFGSGVDQLVEII 250  
 ||||| ||||| ||||| ||||| |||||

Qy 281 KVLGTPREQIREMNPNTYEFKPPQIKAHPTWKVFRPRTPEALCSRLLEYTPTARLT 340  
 ||||| ||||| ||||| ||||| |||||

Db 251 KVLGTPREQIREMNPNTYEFKPPQIKAHPTWKVFRPRTPEALCSRLLEYTPTARLT 310  
 ||||| ||||| ||||| ||||| |||||

Qy 341 PLEACAHSPFDELDRPNVHPNGRDTPL 369  
 ||||| ||||| ||||| ||||| |||||

Db 311 PQACQAHAFDELDRPNVHPNGRDTPL 339  
 ||||| ||||| ||||| ||||| |||||

## RESULT 10

S51105

shaggy protein kinase 4 (EC 2.7.1.1) - garden petunia

N;Alternate names: shaggy/zeeste-white 3 protein kinase homolog

C;Species: Petunia x hybrida (garden petunia)

C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
 C;Accession: S51105

R;Decroocq-Ferrant, V.; van Went, J.; Bianchi, M.W.; de Vries, S.; Kreis, M.

submitted to the EMBL Data Library, December 1994

A;Description: Petunia hybrida homologues of shaggy/zeeste-white 3 expressed in female ar

A;Reference number: S51105

A;Accession: S51105

A;Molecule type: mRNA

A;Residues: 1-409 <DEC>

A;Cross-references: UNIPROT:Q40886; UNIPARC:UPI00000AA695; EMBL:X83619; NID:G619893; PID

C;Genetics:

A;Gene: PSK4

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; protein kinase

F;72-332/Domain: protein kinase homology <KIN>  
 F;80-88/Region: protein kinase ATP-binding motif  
 F;103/Active site: Lys #status predicted

Query Match 62.3%; Score 1296; DB 2; Length 409;  
 Best Local Similarity 62.3%; Pred. No. 7.1e-55;  
 Matches 254; Conservative 49; Mismatches 75; Indels 30; Gaps 7;

Qy 4 MPMEGGGMSGRPRRTTSPAESCKPVQPSAFSGSMKVSQDK-----DQSK----- 46  
 ||||| ||||| ||||| ||||| |||||

Db 6 MPSAG---CKIRTDAMLVD---KLPEEINEMKIRDDKABKEMEAAVVDGNGTEKGHII 57  
 ||||| ||||| ||||| ||||| |||||

Qy 47 VTTVATPGQPRPQEVSYTDTKVINGSGVYQAKLDCSGELVAIKVQLDQKRNK 106  
 ||||| ||||| ||||| ||||| |||||

Db 58 VTTI---GGKNGEPKQITISYMAERVVGQSGFVQAKCLETGETVAIKVQLDQKRYNR 114  
 ||||| ||||| ||||| ||||| |||||

Qy 107 ELQIMRKLDHNCNIVRLRYFFYSSEKDEVLNLDVVPETVYRVARHYSRAKQTLPIVI 166  
 ||||| ||||| ||||| ||||| |||||

Db 115 ELQIRLLDHPNVVALHCHCFSTTE-KDELYLNLDVLEVPETVYRVARHYSKANQQPMI 173  
 ||||| ||||| ||||| ||||| |||||

Qy 167 YVKLYMYQLFRSLAYIHSFGICHRDIKPNQLLLDPTAVLKLCDFGSAKQLVRGPNVSY 226  
 ||||| ||||| ||||| ||||| |||||

Db 174 YVKLYTYQIFRALAYIHGICVCHRDIKPNQLLVNPHTHQLKLCDFGSAKVLKGEPNISY 233  
 ||||| ||||| ||||| ||||| |||||

Qy 227 ICSTRYRAPELIFGATDTSIDVWSAGCVLAELLLGQIPFGSGVDQLVEIIVKLGTP 286  
 ||||| ||||| ||||| ||||| |||||

Db 234 ICSTRYRAPELIFGATDTSIDVWSAGCVLAELLLGQIPFGSGVDQLVEIIVKLGTP 293  
 ||||| ||||| ||||| ||||| |||||

Qy 287 TRSQIREMNPNTYEFKPPQIKAHPTWKVFRPRTPEALCSRLLEYTPTARLTPLAACA 346  
 ||||| ||||| ||||| ||||| |||||

Db 294 TREIKSMNPNTYEFKPPQIKAHPTWKVFRPRTPEALCSRLLEYTPTARLTPLAACA 353  
 ||||| ||||| ||||| ||||| |||||

Qy 347 HSFEDELDRPNVHPNGRDTPLFNFTTQEL-SSNPPLATILIPPHAR 393  
 ||||| ||||| ||||| ||||| |||||

Db 354 HTFDELDRPNVHPNGRDTPLFNFTTQEL-SSNPPLATILIPPHAR 401  
 ||||| ||||| ||||| ||||| |||||

## RESULT 11

T03601

shaggy protein kinase (EC 2.7.1.1) 6 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
 C;Accession: T03601

R;Takvorian, A.; Schwebel-Dugue, N.; Dornelas, M.C.; Tichtindky, G.; Twell, D.; Kreis, M.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z14970

A;Accession: T03601

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-471 <TAK>

A;Cross-references: UNIPROT:O24139; UNIPARC:UPI00000A7EE6; EMBL:Y08607; PIDN:CAA69899.1

A;Experimental source: cultivar Samsun NN; tissue-type pollen

C;Genetics:

A;Gene: NSK6

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; protein kinase

F;140-401/Domain: protein kinase homology <KIN>

Query Match 61.3%; Score 1275.5; DB 2; Length 471;  
 Best Local Similarity 61.7%; Pred. No. 7.4e-55;  
 Matches 250; Conservative 49; Mismatches 77; Indels 29; Gaps 6;

Qy 11 MSGRPRRTTSPAESCKPVQPSAFSGSMKVSQDK-----DQSK----- 52  
 ||||| ||||| ||||| ||||| |||||

Db 73 MDRPENSEFDE-----LPKEMHEMKIKDEKADSHEDNLKMDPEAVVSGNGTGTGQIIIV 126  
 ||||| ||||| ||||| ||||| |||||

Qy 53 T--PGQPDPRPQEVSYTDTKVINGSGVYQAKLDCSGELVAIKVQLDQKRNKRELQI 110  
 ||||| ||||| ||||| ||||| |||||

Db 127 TTVSGRNGQKQTLISYMAERVVGTSFGTGFQAKCLETGESVAIKVQLDQKRYNRRELQI 186  
 ||||| ||||| ||||| ||||| |||||

Qy 111 MRKLDHNCNIVRLRYFFYSSEKDEVLNLDVVPETVYRVARHYSRAKQTLPIVIYVKL 170  
 ||||| ||||| ||||| ||||| |||||

Db 187 MRTLDPHPNVVVKLRHCFYSTTE-KNEVYLNLDVLEYSVETVYRVARHYSRMNQHMFIIVQL 245  
 ||||| ||||| ||||| ||||| |||||

QY 171 YMQLFRLSLAYIHS-FGI CHRDIKPQNLDDPDTAVLKLCDPGSAKOLVRGPNVSYICS 229  
DB 246 YTYQICRALNYMHGLVGVCHRDIKPQNLDDPDTAVLKLCDPGSAKOLVRGPNVSYICS 305  
QY 230 RYTRAPELIFGATDYTSSIDVWSAGCVLAELLLGQIPFGSDGVDQLVEIKVLGTPTRE 289  
DB 306 RYTRAPELIFGATDYTSSIDVWSAGCVLAELLLGQIPFGSDGVDQLVEIKVLGTPTRE 365  
QY 290 QIREMNPNTYEFKPPQIKAHPTWKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSF 349  
DB 366 EIRCMNPNTYEFKPPQIKAHPTWKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSF 425  
QY 350 FDELDRNVKHPNGRDTPALNFTTQELSSNP-PLATILIPPHAR 393  
DB 426 FDLREPNACLNGRPLPLFNFTTAQELSGAPADLRKRLIPEHMR 470

RESULT 12  
T02297  
shaggy protein kinase (EC 2.7.1.1) 91 [similarity] - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: T02297  
Biochim. Biophys. Acta 1442, 261-273, 1998  
R;Tichinsky, G.; Tavaras, R.; Takvorian, A.; Schwebel-Dugue, N.; Twell, D.; Kreis, M.  
A;Title: An evolutionary conserved group of plant GSK-3/shaggy like protein kinase genes  
A;Reference number: Z14641; MUID:99023747; PMID:9804971  
A;Accession: T02297  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-471 <TIC>  
A;Cross-references: UNIPROT:O82029; UNIPARC:UPI000000A3A90; EMBL:AJ224163; NID:G32326114;  
A;Experimental source: cultivar Sameun NN; tissue-type pollen  
C;Genetics:  
A;Gene: NSK 91  
A;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphotransferase; protein kinase  
F;140-401/Domain: protein kinase homology <KIN>

Query Match 61.2%; Score 1273.5; DB 1; Length 471;  
Best Local Similarity 60.5%; Pred. No. 9.3e-54;  
Matches 257; Conservative 42; Mismatches 83; Indels 43; Gaps 7;  
QY 2 EYPMEGG-----MSGRPTTSFAESCKPVQPSAFSGSMKVSVDKDGSK----- 46  
DB 56 EDMPTSGKTTGTSTMDTRPENSEPDE-----LPKEMHEMKIKDEKTDSDHEDNLKDM 109  
QY 47 -----VTTVATPGQGPDRPQEVSYTDTKVINGSGVGVVQAKLCDSGE 90  
DB 110 EPAVSGNGTETGQIIVTTVSGRNGQ---QKTLUSYMAERVVGSGFTVFQAKCLETGE 166  
QY 91 LVAIKVQLQDRKFNRELQIMRKLDHCNIVRLRYFFYSSEKKEDEVYLNVLVDVVPETVY 150  
DB 167 SVAIKVQLQDRRYKNRELQIMRTPDHPNVVVKLRHCFYSTTE-KNEVYLNVLVLEYSVTV 225  
QY 151 RVARHYSRAKQTLPLVIVKLYMYQLFRSLAYIHS-FGI CHRDIKPQNLDDPDTAVLKLCD 209  
DB 226 RVSRHYSRINQHMPIIYVQLYTYQICRALNYMHGLVGVCHRDIKPQNLDDPDTAVLKLCD 285  
QY 210 DFGSAKOLVRGPNVSYICSRYRPAELIFGATDYTSSIDVWSAGCVLAELLLGQIPFG 269  
DB 286 DFGSAKOLVRGPNVSYICSRYRPAELIFGATDYTSSIDVWSAGCVLAELLLGQIPFG 345  
QY 270 DSGVDQLVEIKVLGTPTREQIREMNPNTYEFKPPQIKAHPTWKVFRPRTPEPAIALCSR 329  
DB 346 ESGVDQLVEIKVLGTPTREIRCMNPNTYEFKPPQIKAHPTWKVFRPRTPEPAIALCSR 405  
QY 330 LLETPTARLTPLEACAHSPFDELDRNVKHPNGRDTPALNFTTQELSSNP-PLATILI 388  
DB 406 LLQVSPTRCTALBACAHSPFDELDRNVKHPNGRDTPALNFTTQELSSNP-PLATILI 465  
QY 389 PPHAR 393

DB 466 PEHMR 470

RESULT 13  
T48637  
protein kinase MSK-3-like - Arabidopsis thaliana  
N;Alternate names: protein T15N1.130  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48637  
R;Bevan, M.; Murphy, G.; Ridley, G.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24493  
A;Accession: T48637  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-408 <BEV>  
A;Cross-references: UNIPROT:Q8VZD5; UNIPARC:UPI00000A9FA8; EMBL:AL163792  
A;Experimental source: cultivar Columbia; BAC clone T15N1  
C;Genetics:  
A;Map position: 5  
A;Introns: 39/3; 70/3; 90/3; 181/3; 206/3; 225/3; 272/3; 289/3; 321/3; 349/3; 382/1  
A;Note: T15N1.130  
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 60.8%; Score 1265; DB 2; Length 408;  
Best Local Similarity 65.5%; Pred. No. 2.1e-53;  
Matches 247; Conservative 48; Mismatches 66; Indels 16; Gaps 7;  
QY 30 PSAFGSMKYSRDK-----DGSKVTT---VATPGQGPDRP-QEVSYTDTKVINGSGF 78  
DB 27 PGINEMKIKDDKEMAAVVDGNGTGTGHIIVTTIGKNGQPKQTSYMAERIVGQGSFG 86  
QY 79 VYQAKLCDSGELVAIKVQLQDRKFNRELQIMRKLDHCNIVRLRYFFYSSEKKEDEVYLN 138  
DB 87 IVFQAKCLETGETVAIKVQLQDRKFNRELQIMRKLDHCNIVRLRYFFYSSEKKEDEVYLN 145  
QY 139 NLVLDVVPETVYVARHYSRAKQTLPLVIVKLYMYQLFRSLAYIHS-FGI CHRDIKPQNL 197  
DB 146 NLVLDVVPETVYVARHYSRAKQTLPLVIVKLYMYQLFRSLAYIHS-FGI CHRDIKPQNL 205  
QY 198 LLDPDPTAVLKLCDPGSAKOLVRGPNVSYICSRYRPAELIFGATDYTSSIDVWSAGCVL 257  
DB 206 LVNPHTHQVQLCDPGSAKOLVRGPNVSYICSRYRPAELIFGATDYTSSIDVWSAGCVL 265  
QY 258 AELLGQIPFGSDGVDQLVEIKVLGTPTREQIREMNPNTYEFKPPQIKAHPTWKVFRP 317  
DB 266 AELLGQIPFGSDGVDQLVEIKVLGTPTREIRCMNPNTYEFKPPQIKAHPTWKVFRP 325  
QY 318 RTPPEALCSRLLEYTPPTARLTPLEACAHSPFDELDRNVKHPNGRDTPALNFTTQEL 377  
DB 326 RTPPEAVDLVSRLLQVSPNLRST-AAIVHPFPFDELDRNVKHPNGRDTPALNFTTQEL 383  
QY 378 -SSNPPLATILIPPHAR 393  
DB 384 KGASLELLSKLIPDHAR 400

RESULT 14  
T01236  
serine/threonine-specific protein kinase (EC 2.7.1.1) F6N23.11 [similarity] - Arabidopsis  
N;Alternate names: protein F6N23.11; shaggy-related protein kinase tetha  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: T01236  
R;Geisel, C.  
submitted to the EMBL Data Library, April 1998  
A;Description: The sequence of A. thaliana F6N23.  
A;Reference number: Z14281  
A;Accession: T01236  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA

A;Residues: 1-472 <GI>  
A;Cross-references: UNIPROT:Q96287; UNIPARC:UPI0000000E6A; EMBL:AF058919; NID:g3047100;  
C;Genetics:  
A;Gene: ATSP:F6N23.11  
A;Map position: 5  
A;Introns: 21/3; 103/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3;  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphotransferase; protein kinase  
F;136-397/Domain: protein kinase homology <KIN>  
F;144-152/Region: protein kinase ATP-binding motif  
F;167/Active site: Lys #status predicted

Query Match 60.58; Score 1258; DB 1; Length 472;  
Best Local Similarity 61.6%; Pred. No. 5e-53;  
Matches 250; Conservative 54; Mismatches 74; Indels 28; Gaps 9;

Qy	10	GMGRPRRTTSFAESCKPV--QPSAFGSMKV-----SRDKD-----GSKVTVV	51
Db	67	GTSNVP-----AVSEKPVDDQLPDVMIEMKIRDERNANREDKMETTVVNGSGTGTQVI	121
Qy	52	ATPGQGPDRP-QEVSYTDTKVINGSGFVYVYQAKLDCSGLVAIKKVLQDKRPFKNRELQ	109
Db	122	TTTVGGRDGRPKQTISTYMAERVVGSGFVYVYQAKLDCSGLVAIKKVLQDKRPFKNRELQ	181
Qy	110	MRKLDHCNIVRLRYFFYSSEKDEVLNLVDVVPETVYVARHYSRAKQTLPIVYVK	169
Db	182	IMRLQHPNVVRLRHSPFTTD-KDELYLNLVLEVPETVYVARHYSRAKQTLPIVYVK	240
Qy	170	LYMYQLFRSLAYTH-SFGICHRDIKPNQNLDPDTAVLKLDCFSAGKOLVRGEPNVSYIC	228
Db	241	LYTYQICRALYVLRVVGCHRDIKPNQNLDPDTAVLKLDCFSAGKOLVRGEPNVSYIC	300
Qy	229	SRYRAPELIFGATDYTSSIDVMSAGCVLAELLIGQPIFFPGDSGVDDQLVEIKVLGTPTR	288
Db	301	SRYRAPELIFGATEYTNADMWSGCVMAELLIGQPIFFPGDSGVDDQLVEIKVLGTPTR	360
Qy	289	EQIREMNPNTYEFKFPQIKAHPTWKVFRPTPEAIALCSRLLLEYTPTARLTPLACAHNS	348
Db	361	EEIRCMNPNTYEFKFPQIKAHPTWKVFRPTPEAIALCSRLLLEYTPTARLTPLACAHNS	420
Qy	349	FDLDRDPNVKHPNGRDTPALFNFTTQELS-SNPPLATILIPPHAR	393
Db	421	FFDLDLPNVSLNPGRALPPLFNFTTQELAGASTELRQLIPAHQ	466

RESULT 15

S37642  
protein kinase MSK-3 (EC 2.7.1.-) [similarity] - alfalfa  
C;Species: Medicago sativa (alfalfa)  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
C;Accession: S37642  
R;Pay, A.; Jonak, C.; Boegre, L.; Meskiane, I.; Mairinger, T.; Szalay, A.; Heberle-Bors,  
plant J. 3, 847-856, 1993  
A;Title: The MSK family of alfalfa protein kinase genes encodes homologues of shaggy/gly  
A;Reference number: S37642; MUID:94004996; PMID:8401615  
A;Accession: S37642  
A;Molecule type: mRNA  
A;Residues: 1-412 <PAY>  
A;Cross-references: UNIPARC:UPI000016D9F3; EMBL:X68409; NID:g311147; PIDN:CAA48472.1; PI  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;73-334/Domain: protein kinase homology <KIN>  
F;81-89/Region: protein kinase ATP-binding motif  
F;104/Active site: Lys #status predicted

Query Match 60.4%; Score 1256; DB 1; Length 412;  
Best Local Similarity 61.2%; Pred. No. 5.5e-53;  
Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

Qy	6	MEGGGMSGRPRRTTSFAESCKPV--QPSAFGSMKVSRDK-----DGSKVTT---VV	51
Db	2	MASGGVA--PASGFIDKNASSGVGEKLPPEWMDKRDCKEMEAAITVDGNGTGTGHIV	59

Qy	52	ATPGQGPDRP-QEVSYTDTKVINGSGFVYVYQAKLDCSGLVAIKKVLQDKRPFKNRELQ	110
Db	60	TTTGGKNGQPKQTISTYMAERVVGSGFVYVYQAKLDCSGLVAIKKVLQDKRPFKNRELQ	119
Qy	111	MRKLDHCNIVRLRYFFYSSEKDEVLNLVDVVPETVYVARHYSRAKQTLPIVYVK	170
Db	120	MRLLDHPNVVSLKHCFESTTE-KDELYLNLVLEVPETVYVARHYSRAKQTLPIVYVK	178
Qy	171	YMYQLFRSLAYTH-SFGICHRDIKPNQNLDPDTAVLKLDCFSAGKOLVRGEPNVSYIC	229
Db	179	YSYQICRALYVLRVVGCHRDIKPNQNLDPDTAVLKLDCFSAGKOLVRGEPNVSYIC	238
Qy	230	RYRAPELIFGATDYTSSIDVMSAGCVLAELLIGQPIFFPGDSGVDDQLVEIKVLGTPTR	289
Db	239	RYRAPELIFGATEYTNADMWSGCVLAELLIGQPIFFPGDSGVDDQLVEIKVLGTPTR	298
Qy	290	QIREMNPNTYEFKFPQIKAHPTWKVFRPTPEAIALCSRLLLEYTPTARLTPLACAHNS	349
Db	299	EIKCMNPNTYEFKFPQIKAHPTWKVFRPTPEAIALCSRLLLEYTPTARLTPLACAHNS	358
Qy	350	FDLDRDPNVKHPNGRDTPALFNFTTQELS-SNPPLATILIPPHAR	393
Db	359	YDDVRDPNTRLPNGRFLPLFNFKVKNELKGVPAEMLVKLVPPHAR	403

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Job time : 42 secs

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